

STIC-Biotech/ChemLib

88239

From: Gibbs, Terra
Sent: Wednesday, March 05, 2003 2:05 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

Could you please do a regular search of SEQ ID NO:1 of USSN 09/909775?

Please no EST's and no interference search.

Terra Gibbs #79523
AU 1635
Mailbox 11E12
306-3221

CRFE

THANK YOU!

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 3/4/03
Date Completed: 3/13/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH: /
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

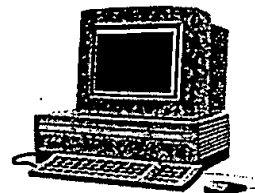
VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 03
WWW/Internet: _____
Other (specify): _____

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BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information C

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or* contact:

Mary Hale, Supervisor, 308-4:
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.gov v

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 06:16:28 ; Search time 7138 Seconds
(without alignments)
11575.072 Million cell updates/sec

Title: US-09-909-775-1
Perfect score: 2839
Sequence: 1 agcgccgctgaattctagg.....taacatctcacggaattc 2839

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2839	100.0	2839	6	AX418513 Sequence
2	2839	100.0	2840	9	AF026692 Homo sapi
3	1876.2	66.1	2009	6	AR129250 Sequence
4	1704.6	60.0	1767	6	E28891 Member of F
5	1704.6	60.0	1767	6	E41285 Member of F
6	1694.8	59.7	1969	6	E28892 Member of F
7	1694.8	59.7	1969	6	E41286 Member of F
8	1569.8	55.3	174241	9	AC018634 Human Chr
9	1556.2	54.8	225912	2	AC084210 Homo sapi
10	1392.8	49.1	1458	6	E28726 Novel human
11	1392.8	49.1	1458	6	E46935 Novel human
12	936	33.0	1910	10	AF012891 Rattus no
13	920.2	32.4	1785	10	AF117709 Mus muscu
14	918.2	32.3	1739	10	BC034853 Mus muscu
15	906.8	31.9	1715	10	AF140346 Rattus no
16	731	25.7	2896	10	AF220608 Rattus no
17	700.2	24.7	185202	2	AC120781 Pan trogl
18	700.2	24.7	241570	2	AC120839 Pan trogl
19	690.4	24.3	195280	9	AC073869 Homo sapi
20	540.6	19.0	584	6	AX393842 Sequence
21	519.8	18.3	547	6	AX062436 Sequence
22	519.8	18.3	547	6	AX367353 Sequence
23	515.8	18.2	544	6	AX360472 Sequence
24	480.8	16.9	512	6	AX360334 Sequence
25	477.4	16.8	566	6	AX260813 Sequence
26	444.8	15.7	448	6	AX329897 Sequence
27	444.8	15.7	448	6	AX335458 Sequence
28	433.8	15.3	445	6	AX393881 Sequence
29	421	14.8	7323	6	AX344800 Sequence
30	420	14.8	7323	6	AX344801 Sequence
31	395.8	13.9	401	6	AX365884 Sequence
32	390	13.7	130291	2	AC112580 Rattus no
33	387.8	13.7	3357	10	AF364906 Mus muscu
34	387.8	13.7	213110	2	AC087324 Mus muscu
35	387.8	13.7	231938	2	AC079025 Mus muscu
36	386.8	13.6	208398	2	AC123245 Rattus no
37	383.2	13.5	4483	10	AF140347 Rattus no
38	374.8	13.2	1050	10	MMU88569 Mus musculu
39	356.2	12.5	137159	2	AC069090 Homo sapi
40	312.8	11.0	1833	5	AF218057 Gallus ga
41	306.2	10.8	323	6	AX393671 Sequence
42	305.4	10.8	2351	4	BTU24164 Bos taurus
43	303.6	10.7	378	6	AX261130 Sequence
44	295.2	10.4	1786	10	MMU91905 Mus musculu
45	295.2	10.4	2176	6	AR116407 Sequence

ALIGNMENTS

RESULT 1	AX418513	Sequence 1 from Patent WO0205857.	2839 bp	DNA	linear	PAT 18-JUN-2002
AX418513	Sequence 1 from Patent WO0205857.	2839 bp	DNA	linear	PAT 18-JUN-2002	
LOCUS	AX418513	Sequence 1 from Patent WO0205857.	2839 bp	DNA	linear	PAT 18-JUN-2002
DEFINITION	AX418513	Sequence 1 from Patent WO0205857.	2839 bp	DNA	linear	PAT 18-JUN-2002
ACCESSION	AX418513	Sequence 1 from Patent WO0205857.	2839 bp	DNA	linear	PAT 18-JUN-2002
VERSION	AX418513.1	GI:21523378				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE						
AUTHORS	Schiavi, S., Madden, S.L., Manavalan, P., Levine, M. and de Beur, S.J.					
TITLE	Phosphatoin-related gene and methods of use thereof					
JOURNAL	Patent: WO 0205857-A 1 24-JAN-2002;					

GENZYME CORPORATION (US)		Db		721		CACACCAGACATGATGGTACAGAAAGGCCCTTGTATGTTGACTGTAAACGCTTAAGCCC		780	
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BASE COUNT	807 a	624 c	649 g	759 t					
ORIGIN									
Query Match	100.0%;	Score 2839;	DB 6;	Length 2839;					
Best Local Similarity	100.0%;	Pred. No. 0;							
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QY	1	ACGGCGCGCTGAATTTAGGGCGGGTTCGGCGCCCGAAGGCTGAGAGCTGGCGTGTGCTG	60						
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DB	301	GGCGCTGGCGTGGCGGGCGGCCCTGCGAGGGGGTGGCATCCCTATGTGCGGGCACAT	360						
QY	361	GGCTTGAACATCAGCGGGATGCCAACACCTGCACACAGCAGCAGGAGAACGCCAT	420						
DB	361	GGCTTGAACATCAGCGGGATGCCAACACCTGCACACAGCAGCAGGAGAACGCCAT	420						
QY	421	CTTGGCCATCGACGAGTACAGAGCTGGTGGACGTGAACCTGCAGCGCGCTGCTGGCCTT	480						
DB	421	CTTGGCCATCGACGAGTACAGAGCTGGTGGACGTGAACCTGCAGCGCGCTGCTGGCCTT	480						
QY	481	CTTCTCTGTGCCATGTACGCGGCCATTTCACCCCTGGAGTTCCTGCAGCACCCCTATCAA	540						
DB	481	CTTCTCTGTGCCATGTACGCGGCCATTTCACCCCTGGAGTTCCTGCAGCACCCCTATCAA	540						
QY	541	GGCGTGAAGTGGTGTGCCAACGGCGCGGACGACTGCGAGCGCCCTCATGAAGATGTA	600						
DB	541	GGCGTGAAGTGGTGTGCCAACGGCGCGGACGACTGCGAGCGCCCTCATGAAGATGTA	600						
QY	601	CAACACAGCTGGCGGAAAGCCTGGCCTGCGAGGAGCTGCCTGTCTATGACCGTGGCGT	660						
DB	601	CAACACAGCTGGCGGAAAGCCTGGCCTGCGAGGAGCTGCCTGTCTATGACCGTGGCGT	660						
QY	661	GTGCATTTCCGCTGAAGCCATCTGCAGGACCTCCCGGAGGATGTTAAGTGGATGACAT	720						
DB	661	GTGCATTTCCGCTGAAGCCATCTGCAGGACCTCCCGGAGGATGTTAAGTGGATGACAT	720						
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Qy	1921	GAACCTTAAACAAAAATAATAATAAAGAAAAATAAATAAAGAGGAGGAGGAGCAATG	1980
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Qy	1981	TCTGATTCCTGTTTTTGGTTACCTGATTTCCATGATCATGATGCTTCTTGTCAACACC	2040
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Qy	2041	CTCTTAAGCAGCAGCAGCAAGAGTGTGCTGTACCATTAAGAGTTAGTACTAAT	2100
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Qy	2581	TCTCCAGGTGTTGCTTATGCACTTATAAATGATTGAACAATAAATACTAGGAACCTG	2640
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Db	2641	TATACATGTTTTCATACACCTGCCCTTGTGTTGCTTGGCCCTTTTATGAGATAAGTTTCT	2700
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Db	2821	AAACATCTCACCGGAATTC	2839
RESULT 2			
AF026692			

LOCUS	AF026692	2840 bp	mRNA	linear	PRI 02-MAR-1998
DEFINITION	Homo sapiens frizzled related protein frpHE mRNA, complete cds.				
ACCESSION	AF026692				
VERSION	AF026692.1	GI:2920803			
KEYWORDS	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2840)				
AUTHORS	Abu-Jawdeh, G.M., Comella, N., Brown, L.F., Tognazzi, K. and Kocher, O.				
TITLE	frizzled related protein frpHE (Homo Sapiens)				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 2840)				
AUTHORS	Abu-Jawdeh, G.M., Comella, N., Brown, L.F., Tognazzi, K. and Kocher, O.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-SEP-1997) Pathology, BIDMC, East Campus, 330 Brookline Avenue, Boston, MA 02215, USA				
REFERENCE	3 (bases 1 to 2840)				
AUTHORS	Abu-Jawdeh, G.M., Comella, N., Brown, L.F., Tognazzi, K. and Kocher, O.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-MAR-1998) Pathology, BIDMC, East Campus, 330 Brookline Avenue, Boston, MA 02215, USA				
REMARK	Sequence update by submitter				
COMMENT	On Mar 2, 1998 this sequence version replaced gi:2576419.				
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Db	122	GACTGGAGTTGGGGGAGAGAACTCTCTGCGCCCGCAGAGATTTCTCTCGGCGAAG	181		
Qy	181	GACACGGAAGATGAGGTGGCAGAGAGAGGCGCTTCTGTCTGCGGGGTGCGACG	240		
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QY 1021 CATCATGTGTTAGGAGTGGCGTTCAAGGATGATGCTTCTTGAAATTTGCTTAGTTGAAA 1080
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QY 1141 GAGACAGTTCAGGACAGAAAGAACAGCCGGGCGCCACCTCGTAGTAATCCCCCAA 1200
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RESULT 4
E28891
LOCUS E28891 1767 bp DNA linear PAT 18-JUN-2001
DEFINITION Member of FR2B family, FRAZZLED.
ACCESSION E28891
VERSION E28891.1 GI:13025478
KEYWORDS JP 1999000186-A/1.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1767)
AUTHORS Michael,W.L., Ian,E.J. and Sanjay,K.
TITLE Member of FR2B family, FRAZZLED
JOURNAL Patent: JP 1999000186-A 1 06-JAN-1999;
SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 1999000186-A/1
PD 06-JAN-1999
PF 22-MAY-1998 JP 1998141081
PR 22-MAY-1997 US 60/047408,26-NOV-1997 US 08/978981 PI
MICHAEL WILLIAM LARK, IAN EDWARD JAMES, SANJAY KUMAR PC
C12N15/09,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00, PC
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Query Match 60.0%; Score 1704.6; DB 6; Length 1767;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1754; Conservative 0; Mismatches 9; Indels 4; Gaps 4;
QY 88 CGCGCGCGGACCGCGCGCGCGCGCGCTTTGCTGCGGACTGGAGTTTGGGGAGAAACTCTC 147
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RESULT 5
E41285
LOCUS E41285 1767 bp DNA linear PAT 31-JAN-2002
DEFINITION Member of FR2B family, FRAZZLED.
ACCESSION E41285
VERSION E41285.1 GI:18625155
KEYWORDS JP 2000083683-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1767)
AUTHORS Lark,M.W., James,I.E. and Kumar,S.
TITLE Member of FR2B family, FRAZZLED

JOURNAL Patent: JP 2000083683-A 1 28-MAR-2000;
COMMENT SMITHKLINE BEECHAM CORP
OS Unidentified
PN JP 2000083683-A/1
PD 28-MAR-2000
PF 17-AUG-1999 JP 1999230635
PR 22-MAY-1997 US 60/047408, 26-NOV-1997 US 08/978981 PI
MICHAEL WILLIAM LARK, IAN EDWARD JAMES, SANJAY KUMAR PC
C12N15/09, A61K31/7088, A61K38/00, A61K39/00, A61K39/395, PC
A61K39/395, A61K45/00,
PC A61K48/00, A61P7/00, A61P13/12, A61P17/06, A61P19/02, A61P19/10, PC
A61P25/28,
PC A61P29/00, A61P31/00, A61P35/00, A61P37/06, C07K14/47, C07K16/18,
PC C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P1/68, G01N33/53, PC
G01N33/531,
PC G01N33/566, G01N33/577//C12P21/08, C12N15/00, A61K37/02, C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key 1. .1767 Location/Qualifiers
FT source 1. .1767 /organism='Unidentified'.
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1754; Conservative 0; Mismatches 9; Indels 4; Gaps 4;
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QY 1914 TTAG 1917
Db 1941 TTGG 1944
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RESULT 7
LOCUS E41286
DEFINITION Member of PRZB family, FRAZZLED.
ACCESSION E41286
VERSION E41286.1 GI:18625156
KEYWORDS JP 2000083683-A/2.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1969)
AUTHORS Lark,M.W., James,I.E. and Kumar,S.
TITLE Member of PRZB family, FRAZZLED
JOURNAL Patent: JP 2000083683-A 2 28-MAR-2000;
SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 2000083683-A/2
PD 28-MAR-2000
PR 17-AUG-1999 JP 1999230635
PI 22-MAY-1997 US 60/047408, 26-NOV-1997 US 08/978981 PI
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C12N15/09, A61K31/7088, A61K38/00, A61K39/00, A61K39/395, PC
A61K39/395, A61K45/00,
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PC C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/68, G01N33/53, PC
G01N33/531,
PC G01N33/566, G01N33/577//C12P21/08, C12N15/00, A61K37/02, C12N5/00

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CC Strandedness: Single;
CC Topology: Linear;
FH Key 1. 1969 Location/Qualifiers
FT source /organism="Unidentified".
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1. 1969
BASE COUNT 504 a 484 c 518 g 458 t 5 others
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Query Match 59.7% Score 1694.8; DB 6; Length 1969;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1854; Conservative 0; Mismatches 49; Indels 21; Gaps 11;

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QY 1914 TTAG 1917
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Db 1941 TTTG 1944

RESULT 8

AC018634

LOCUS

DEFINITION

AC018634

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC018634 174241 bp DNA linear PRI 28-JUL-2000
Human Chromosome 7 clone RP11-243E12, complete sequence.

AC018634

AC018634.3 GI:9558607

HTG.

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 174241)

Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and

Olson,M.V.

Large-scale Mapping and Sequencing of Human Chromosome 7

Unpublished

2 (bases 1 to 174241)

Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.

Direct Submission

Submitted (15-DEC-1999) Human Genome Center, University of

Washington, Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 174241)

Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and

Olson,M.V.

Direct Submission

Submitted (28-JUL-2000) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

On Jul 28, 2000 this sequence version replaced gi:8050915.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu/UWGC/>

Contact: uwgchgs@u.washington.edu

----- Project Information

Center project name: HsaChr7

Center clone name: RP11-243E12 (djs156)

----- Summary Statistics

Sequencing vector: M13; X02513; 100% of reads

Chemistry: Dye-primer-amersham; 66% of reads

Chemistry: Dye-terminator ET-amersham; 34% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 173493 bases at least Q40

Consensus quality: 174139 bases at least Q30

Consensus quality: 174231 bases at least Q20

Insert size: 179271; 8.6% error; agarose-fp

Insert size: 174241; sum-of-contigs

Quality coverage: 6.32x in Q20 bases; agarose-fp

Quality coverage: 6.50x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-605P22 (UWGC:djs708)

3': Mapping in progress

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

all regions were either double-stranded or sequenced with an

alternate chemistry or covered by high quality data (i.e., Phred

quality >= 30); an attempt was made to resolve all sequencing

problems, such as compressions and repeats; all regions were

covered by at least one plasmid subclone or more than one M13

subclone; and the assembly was confirmed by restriction digest.

Double stranded (DS) coverage: 70.2%
DS or two chemistry coverage: 29%
Single stranded regions: 0.787% in 7 gaps

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.

The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)

are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

BglII EcoRI

SeqDerMap FngPrnt SeqDerMap FngPrnt

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Best Local Similarity 98.1%; Pred. NO. 5e-290;
Matches 1694; Conservative 0; Mismatches 22; Indels 11; Gaps 10;

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QY 1232 GCCAGTCCCAAGAGAACATTAACACTAGGAGTGCCGAGAGAGAACAAACCCGAAAGA 1291
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QY	1412	GCTCTTCATAGACACATCTTCAGCATTTTCTTAAGCTATGCTTCAGTTTCTCTTGT	1471
Db	85867	GCTCTTCATAGACACATCTTCAGCATTTTCTTAAGCTATGCTTCAGTTTCTCTTGT	85926
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Db	86586	CCAGAAGAGAGGATATGCTACTCATCTTACTTCCAGGAGATCCACCTCAGAGTAATTTTG	86645
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* 223432 223531: gap of unknown length
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FEATURES

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Matches 1692; Conservative 0; Mismatches 23; Indels 12; Gaps 11;
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RESULT 10
E28726
LOCUS E28726
DEFINITION Novel human gene (ATG-1639) similar to secretory protein Frizb.
ACCESSION E28726
VERSION E28726.1 GI:13025446

KEYWORDS JP 1999004698-A/1.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1458)
AUTHORS Ading, F. and Yuan, Z.
TITLE Novel human gene (ATG-1639) similar to secretory protein Frizb
JOURNAL Patent: JP 1999004698-A 1 12-JAN-1999;
SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 1999004698-A/1
PD 12-JAN-1999
PF 25-MAY-1998 JP 1998142888
PR 23-MAY-1997 US 60/047626.14-JUL-1997 US 08/892083 PI
ADING FU, YUAN ZU
PC C12N15/09, A61K31/70, A61K38/00, A61K39/00, A61K39/395, A61K39/395,
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C12N5/10, C12P21/02,
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RESULT 12
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LOCUS AF012891 1910 bp mRNA linear ROD 03-AUG-1997
DEFINITION Rattus norvegicus frizzled related protein frpAP mRNA, complete cds.
ACCESSION AF012891
VERSION AF012891.1 GI:2293563
KEYWORDS
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
REFERENCE 1 (bases 1 to 1910)
AUTHORS Guo,K., Wolf,V., Dharmarajan,A., Feng,Z., Bielke,W., Susanne,S. and Friis,R.R.
TITLE Apoptosis-associated Gene Expression in Corpus luteum of the Rat
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Unpublished
2 (bases 1 to 1910)
Wolf,V., Artuso,L., Dharmarajan,A., Guo,K., Bielke,W. and Friis,R.R.
A frizzled related Gene is upregulated in Physiological Apoptosis
Unpublished
3 (bases 1 to 1910)
Wolf,V., Artuso,L., Dharmarajan,A., Guo,K., Bielke,W. and Friis,R.R.
Direct Submission
Submitted (07-JUL-1997) Department for Clinical Research,
University of Bern, Tiefenaustrasse 120, Bern 3004, Switzerland
Location/Qualifiers
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Query Match 33.0%; Score 936; DB 10; Length 1910;
Best Local Similarity 76.1%; Pred. No. 5.8e-169;
Matches 1311; Conservative 0; Mismatches 341; Indels 71; Gaps 10;
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LOCUS Mus musculus secreted frizzled-related sequence protein 4 (Sfrp4)
DEFINITION mRNA, complete cds.
ACCESSION AF117709
VERSION AF117709.1 GI:4219089
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1785)
AUTHORS Chang J.T., Esumi, N., Moore, K., Li, Y., Zhang, S., Chew, C.,
Goodman, B., Rattner, A., Moody, S., Stetten, G., Campochiaro, P.A. and
Zack, D.J.
TITLE Cloning and characterization of a secreted frizzled-related protein
that is expressed by the retinal pigment epithelium
JOURNAL Hum. Mol. Genet. (1999) In press
REFERENCE 2 (bases 1 to 1785)
AUTHORS Rattner, A. and Nathans, J.H.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-1999) MBG, JHMI, 725 N. Wolfe St., Room 805 PCTB,
Baltimore, MD 21205, USA
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Best Local Similarity 75.1%; Pred. No. 6.1e-166;
Matches 1318; Conservative 0; Mismatches 373; Indels 64; Gaps 11;
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RESULT 14
BC034853
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
Mus musculus, secreted frizzled-related sequence protein 4, clone
MGC:41113 IMAGE:1364770, mRNA, complete cds.
BC034853
BC034853.1 GI:22028397
MGC.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1739)
Strausberg, R.
Direct Submission
Submitted (29-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb-remail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline
Scheln, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 67 Row: b Column: 24
This clone was selected for full length sequencing because it

ACCESSION	AF140348	GI:76724222
VERSION	AF140346.1	

KEYWORDS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1715)
AUTHORS Yam, J.W., Chan, K.W., Wong, V.K. and Hsiao, W.L.
TITLE Transcriptional activity of the promoter region of rat
frizzled-related protein gene
JOURNAL Biochem. Biophys. Res. Commun. 286 (1), 94-100 (2001)
MEDLINE 21378144
PUBMED 11485313
REFERENCE 2 (bases 1 to 1715)
AUTHORS Yam, J.W.P. and Hsiao, W.L.W.
TITLE Regulation of rat frizzled related protein gene
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1715)
AUTHORS Yam, J.W.P. and Hsiao, W.L.W.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1999) Biology, The Hong Kong University of
Science and Technology, Clear Water Bay, Kowloon, Hong Kong, China
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Job time : 8098 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 06:12:49 ; Search time 574 Seconds
(without alignments)
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Title: US-09-909-775-1

Perfect score: 2839

Sequence: 1 agcgccgcgtgaattcagg.....taaacatctcaccggaattc 2839

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2839	100.0	2839	AA141901	Human frizzled rel
2	2839	100.0	2840	AAAS4127	Breast cancer prot
3	2839	100.0	2840	ABQ88233	Human osteoblast d
4	2837.4	99.9	2840	AAA97364	Human colorectal c
5	2820	99.3	2820	ABK92118	Prostate cancer-as
6	1876.2	66.1	2009	AAAF80598	Receptor #86 parti
7	1706.2	60.1	1767	AAAC84495	Human FRAZZLED pol
8	1704.6	60.0	1767	AAV80657	Human FRAZZLED pro
9	1694.8	59.7	1969	AAV80658	Partial human FRAZ

10	1694.8	59.7	1969	22	AAC84496	Partial nucleotide
11	1694.8	59.7	1969	24	ABQ88234	Human osteoblast d
12	1541.2	54.3	1581	20	AAQ28656	Full length clone
13	1432	50.4	1556	20	AAZ33454	Human prostate can
14	1392.8	49.1	1458	19	AAV08951	Human ATG-1639 pro
15	1073.6	37.8	1216	24	ABQ54454	Human ovarian anti
16	1041	36.7	1041	21	AAA54128	Breast cancer prot
17	1027.4	36.2	1046	20	AAQ28655	Nucleotide sequenc
18	898.6	31.7	1041	21	AAA99046	Bos taurus Frazzle
19	564.8	19.9	695	24	ABQ57675	Human colon cancer
20	540.6	19.0	584	24	ABK54035	Human head and nec
21	519.8	18.3	547	22	ABF68145	Human lung tumour
22	519.8	18.3	547	24	ABK38056	CDNA encoding clon
23	515.8	18.2	544	24	ABK16044	Human lung tumour
24	480.8	16.9	512	24	ABK15906	Human lung tumour
25	477.4	16.8	566	23	AA57788	CDNA #464 encoding
26	444.8	15.7	448	24	ABL62069	Colon adenocarcino
27	444.8	15.7	448	24	ABL67630	Oesophagus cancer
28	433.8	15.3	445	24	ABK54073	Human head and nec
29	421	14.8	7323	24	ABN80208	Human chemically m
30	420	14.8	7323	24	ABN80209	Human chemically m
31	395.8	13.9	401	21	AAC65973	Human lung cancer-
32	395.8	13.9	401	24	ABL49192	Human lung tumour
33	381.2	13.4	662	24	ABQ59461	Human colon cancer
34	306.2	10.8	323	24	ABK53865	Human head and nec
35	305.4	10.8	2374	19	AAV18253	Bovine growth-indu
36	303.6	10.7	378	23	AA58105	CDNA #781 encoding
37	295.2	10.4	1786	19	AAV13102	Mouse hsfz cDNA.
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39	295.2	10.4	2176	24	AB198691	Mouse ischaemic co
40	295.2	10.4	2441	19	AAV13104	Mouse hsfz cDNA (v
41	295	10.4	363	24	ABL67602	Oesophagus cancer
42	287.8	10.1	1909	19	AAV13101	Human hsfz cDNA.
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45	286.2	10.1	1484	19	AAV18254	Human growth-induc

ALIGNMENTS

RESULT 1
AA141901
ID AAL41901 standard; CDNA; 2839 BP.

XX AAL41901;

AC AAL41901;

XX 03-MAY-2002 (first entry)

DT Human frizzled related protein 4 (FRP-4) cDNA sequence.

DE Human; phosphate homeostasis modulation; frizzled related protein-4;
KW FRP-4; gene; phosphate transportation; serum phosphate concentration;
KW hypophosphataemia; phosphaturia; 1,25-dihydroxy vitamin D deficiency;
KW osteomalacia; phosphate homeostasis related disease;
KW X-linked hypophosphataemia; rickets; oncogenic osteomalacia;
KW rhabdomyolysis; cardiomyopathy; tumoral calcinosis; renal failure;
KW bone mineralisation; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FT CDS 257..1297
FT /tag= a
FT /product= "FRP-4 protein"

FT WO200205857-A2.

XX 24-JAN-2002.

XX 19-JUL-2001; 2001WO-US23014.

XX 19-JUL-2000; 2000US-219365P.

PR 12-JAN-2001; 2001US-261438P.
XX (GENZ) GENZYME CORP.
PA
PI Schlavi S, Madden SL, Manavalan P, Levine M, De Beur SJ;
XX
XX WPI; 2002-179752/23.
DR P-PSDB; AAO14432.
XX
PT Modulating phosphate homeostasis in a subject, for alleviating
PT oncogenic osteomalacia-associated symptoms, comprises altering the
PT activity of frizzled related protein-4 (FRP4) or a gene encoding FRP-4
PT polypeptide
XX
PS Disclosure; Fig 1; 51pp; English.
XX
CC The invention comprises a method for modulating phosphate homeostasis in
CC a subject. The method involves altering the activity of the frizzled
CC related protein-4 (FRP-4), or altering the expression of the FRP-4 gene.
CC Phosphate plays a critical role in many cellular processes essential to
CC normal functionality of the human body. Phosphate homeostasis is
CC primarily regulated by the kidney, largely through variation in renal
CC tubular re-absorption of phosphate. Alterations of the phosphate
CC transporting function of the kidney and subsequent disturbance of serum
CC phosphate concentration often lead to serious biochemical and clinical
CC problems. The method of the invention is useful for modulating phosphate
CC homeostasis in a subject. The method of the invention can be used to
CC alleviate oncogenic osteomalacia-associated symptoms (e.g.
CC hypophosphataemia, phosphaturia, low serum concentrations of 1,25-
CC dihydroxy vitamin D and osteomalacia). The method of the invention can
CC also be used to treat phosphate homeostasis-related diseases (e.g.
CC x-linked hypophosphataemia, rickets, oncogenic osteomalacia,
CC rhabdomyolysis, cardiomyopathy, tumoral calcinosis, renal failure and
CC bone mineralisation). The present CDNA sequence encodes the human
CC frizzled related protein 4 (FRP-4).
XX
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Query Match 100.0%; Score 2839; DB 24; Length 2839;
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 Db 1741 AAAATATAATGTTTTTAAAGAGAACAGTAGTGAATGAATGTTAAAGATCTTTATGTG 1800
 QY 1801 TTTATGCTGTCAGAGAGATTTTCTGATGAAGGGGATTTTTTGAAGAAATTAGAGAAGT 1860
 Db 1801 TTTATGCTGTCAGAGAGATTTTCTGATGAAGGGGATTTTTTGAAGAAATTAGAGAAGT 1860
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 Db 1861 AGCATATGGAATAATATATGTTTTTTTACCAATGACTTCCAGTTCCTGTTTTTAGCTA 1920
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 Db 2041 CTCCTTAAGCAGCAGCAGCAAGAGTGTGCTGTCTACCATTAGGAGTTAGTACTAAT 2100
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 Db 2101 AGTTGGCTAATGCTCAAGTATTTTATACCCAGAGAGGATATGTCATCATCTTACTTTC 2160
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 QY 2821 AAACATCTCACGGAAATTC 2839
 Db 2821 AAACATCTCACGGAAATTC 2839
 RESULT 2
 AAAS4127
 ID AAAS4127 standard; DNA; 2840 BP.
 XX
 AC AAAS4127;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Breast cancer protein BCX2 coding sequence.
 KW Breast cancer; diagnosis; prognosis; detection; screening;
 KW antibody; oestrogen receptor; anti-oestrogen; immune response;
 KW lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN2;
 KW BCN5; BCO2; BCX2; BCX3; BCA2; BCR2; BCJ7; BCY3; human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 258..1298
 FT /*tag= a
 FT /product= BCX2 protein
 XX
 PN W0200055629-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06952.
 XX
 PR 15-MAR-1999; 99US-0268865.
 PR 12-NOV-1999; 99US-0439878.
 PR 12-NOV-1999; 99US-0440370.
 PR 15-NOV-1999; 99US-0440493.
 PR 16-NOV-1999; 99US-0440676.
 PR 16-NOV-1999; 99US-0440677.
 PR 29-NOV-1999; 99US-0450810.
 PR 02-DEC-1999; 99US-0453137.
 PR 08-MAR-2000; 2000US-0453137.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Mack D, Gish KC;
 XX
 DR WPI; 2000-638216/61.
 DR P-PSDB; AAB00193.
 XX
 PT Screening drug candidates for their ability to modulate breast cancer
 PT by contacting the drug to a cell expressing an expression profile gene
 PT and determining modulation of expression of the gene
 XX
 PS Disclosure; Fig 57; 258pp; English.
 CC
 CC New methods for screening drug candidates are described which
 CC comprise adding a drug candidate to a cell that expresses a protein
 CC selected from BCH1, BCA2, BCJ7, BCN1, BCN5, BCQ2, BCQ5, BCR2, BCX2
 CC and BCY3 or their fragments and determining the effect of the drug
 CC on the expression of those proteins. Antibodies to breast cancer
 CC genes (specifically BCH1 or its fragment (BCH1p1 or BCH1p2)) are

CC useful for inhibiting and treating breast cancer in individuals who
CC are non-responsive to anti-oestrogen and positive for oestrogen
CC receptor. Compositions comprising BCh1 or a nucleic acid encoding
CC BCh1 are useful for eliciting an immune response in an individual.
CC The antibodies are also useful for the diagnosis and prognosis of
CC breast cancer and for screening compositions which modulate the
CC breast cancer phenotype. The method allows rapid and simple
CC detection of lymph node metastases.
XX
XX
SQ Sequence 2840 BP; 807 A; 625 C; 649 G; 759 T; 0 other;

Query Match 100.0%; Score 2839; DB 21; Length 2840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCGGCGCTGAATTTCTAGGCGGGTTCGCGCCCGGAGAGCTGAGAGCTGGGCTGCTCG 60
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DB 62 TGGCCCTGTGTGCAGACGCGGAGCTCCGCGGCGGACCCCGGCGCCGCTTTGTGTC 121
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DB 122 GACTGGAGTTTGGGGAAGAACTCTCTGCGCCCGCAGAGATTTCTTCTCGGCGAAG 181
QY 181 GACAGCGAAAGATGAGGTTGGCAGGAAGAGAGGCGCTTCTGTCGCGGGGTGCGACG 240
DB 182 GACAGCGAAAGATGAGGTTGGCAGGAAGAGAGGCGCTTCTGTCGCGGGGTGCGACG 241
QY 241 GCGAGAGGCGAGTGCATGTTCTCTCCATCTCTAGTGGCGCTGTGCTGTGCGTGCACCT 300
DB 242 GCGAGAGGCGAGTGCATGTTCTCTCCATCTCTAGTGGCGCTGTGCTGTGCGTGCACCT 301
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DB 422 CTTGCGCATCGAGCAGTACGAGAGCTGTTGGACGTTGAACCTGCAGCGCGCTGCGGCTT 481
QY 481 CTTCTTCTGTGCCATGACGCGCCCATTTGCAACCTTGGAGTTTCTGCGACGACCCATCAA 540
DB 482 CTTCTTCTGTGCCATGACGCGCCCATTTGCAACCTTGGAGTTTCTGCGACGACCCATCAA 541
QY 541 GCGGTGCAAGTGGTGTGCAAGCGCGCGGAGCTGCGAGCGCTCATGAAGATGTA 600
DB 542 GCGGTGCAAGTGGTGTGCAAGCGCGCGGAGCTGCGAGCGCTCATGAAGATGTA 601
QY 601 CAACACAGCTGGCCGAAGCCTTGGCCCTGCGACAGCTGCCCTGTATGACCGTGGCGT 660
DB 602 CAACACAGCTGGCCGAAGCCTTGGCCCTGCGACAGCTGCCCTGTATGACCGTGGCGT 661
QY 661 GTGCAATTTGCGCTGAAGCCATGTCAGGACCTCCCGGAGGATGTTAAGTGGATGACAT 720
DB 662 GTGCAATTTGCGCTGAAGCCATGTCAGGACCTCCCGGAGGATGTTAAGTGGATGACAT 721
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DB 722 CACACAGACATGATGTTACAGGAAGGCTCTTGTATGTTGACTGTAAAGCGCTAAGCCC 781
QY 781 CGATCGGTGCAAGTGTAAAGGTTGAAGCCAACTTTGGCAACGATATCTCAGCAAAACTA 840
DB 782 CGATCGGTGCAAGTGTAAAGGTTGAAGCCAACTTTGGCAACGATATCTCAGCAAAACTA 841
QY 841 CAGCTATGTTATTCATGCCCAAAATAAAGCTGTGCGAGAGGATGGCTGCAATGAGTGCAC 900

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DB 902 AACCGTGGTGGATGTAAAGAGATCTTCAAGTCCCTCATCACCACATCCCTCGAAGTCAAGT 961
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DB 1202 ACCAAAGGAAAGCCCTCTGCTCCCAACAGCCAGCTGCCCAAGAAACATTAATACTAG 1261
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DB 1322 ACTTCCGACTTCTTACAGGATGAGGCTGGGCAATTCCTTGGGAGACGCTATGTAAAGGCCA 1381
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DB 1562 AGTAACCTGTGTCATCTCTAGAGAGTGGGAAATTAATGCTTCTTCAATTCACCT 1621
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DB 1922 GAACTTAAACAAACAAATAATAATAAGAAAAATAATAAGAGGAGGAGGAGGAGCAATG 1981

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Db 2402 ATTGTGGCAATGTGAGGCAATTTATTTAAACAAATTTATTTGGCCCTTTTGTGTAACAC 2461
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Db 2642 TATACATGTGTTTATACACCTGCCCTTGTCTTGCCCTTTATGAGATAGTTTTCCT 2701
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Db 2762 ACTCAACAAAGTGTGCTATTGATGATCTATTAGTGGTTTCTTCACTGACATATGAT 2821
Oy 2821 AAACATCTCACCGGAATTC 2839
Db 2822 AAACATCTCACCGGAATTC 2840

RESULT 3
ABQ88233
ID ABQ88233 standard; cdna; 2840 BP.
XX
AC ABQ88233;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human osteoblast differentiation related cdna SEQ ID NO 140.
XX
KW Human; osteoblast; stem cell differentiation; bone tissue deposition;
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osteoporosis; osteopathic; ss.
KW
XX
OS Homo sapiens.
XX
PN WO200250301-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-US48276.
XX
PR 18-DEC-2000; 2000US-255882P.
PR 24-APR-2001; 2001US-285691P.
XX
PA (GENE-) GENE LOGIC INC.
PA (PROC ) PROCTER & GAMBLE CO.
XX
PI JI D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
PI Mertz L;
XX
DR WPI; 2002-557663/59.
XX
PT Use of genes and their expression profiles associated with osteoblast
PT differentiation for screening modulators bone formation, for diagnosing
PT or treating e.g. osteoporosis, or as markers for the differentiation
PT process
XX
XX Claim 1; SEQ ID NO 140; 78pp + Sequence Listing; English.
XX
CC The invention relates to genes and their expression profiles are used
CC for:
CC (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition;
CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC osteoblast formation or osteoporosis; or
CC (c) treating or monitoring treatment of the conditions cited in (b), or
CC monitoring the progression of bone tissue deposition.
CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
CC drug-induced abnormalities in bone formation or bone loss, conditions
CC that involve altered bone metabolism (e.g. idiopathic juvenile
CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC osteoblast differentiation associated cdna marker of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2840 BP; 807 A; 625 C; 649 G; 759 T; 0 other;
Query Match 100.0%; Score 2839; DB 24; Length 2840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGCGGCGCGTGAATTCCTAGGCGGGGTTGCGGCCCGAAGGCTGAGAGCTGGCGCTGCTGC 60
Db 2 AGCGGCGCGTGAATTCCTAGGCGGGGTTGCGGCCCGAAGGCTGAGAGCTGGCGCTGCTGC 61
Oy 61 TGCCCTGTGTGCGACAGCGCGAGCTCGCGGCGGAGACCCCGCGGCTTTGCTGCC 120
Db 62 TGCCCTGTGTGCGACAGCGCGAGCTCGCGGCGGAGACCCCGCGGCTTTGCTGCC 121
Oy 121 GACTGGAGTTTGGGGAAGAAACTCTCTGCGGCCCGAAGATTTCTTCCTCGGGAAG 180
Db 122 GACTGGAGTTTGGGGAAGAAACTCTCTGCGGCCCGAAGATTTCTTCCTCGGGAAG 181
Oy 181 GACAGCGAAAGATGAGGTGGCAGGAAGAGCGCTTTCTGTGTCGGGGGTGCGACG 240
Db 182 GACAGCGAAAGATGAGGTGGCAGGAAGAGCGCTTTCTGTGTCGGGGGTGCGACG 241
Oy 241 GCGAGAGGCGAGTGCATGTTCTCTCCATCTAGTGGCGCTGCTGCTGCTGCACCT 300
Db 242 GCGAGAGGCGAGTGCATGTTCTCTCCATCTAGTGGCGCTGCTGCTGCTGCACCT 301
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DB 362 GCGCTGGAAACATCAGCGGATGCCCAACACCTGCACACACGACGCGAGGAGAGCGCCAT 421
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DB 422 CCGTGGCCATCGAGCAGTAGTACGAGGAGCTGGTGACGTGAACCTGCAGCGCGCTCGCGCTT 481
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DB 482 CTTCTTCTGTGCCATGTAGCGGCCCATTTTGACCCCTGGAGTTCCTGCGAGGACCCATCA 541
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DB 542 GCGGTGCAAGTCGGTGTGCCAACGCGCGCGACGACCTGCGAGCGCCCTCATCAAGATGTA 601
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DB 722 CACACACAGATGATGTACAGGAAGCCCTCTGATGTGTGACTCTCAAGCAAAACATA 841
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DB 1442 TTTCTTAAGGCTATGCTTCACTTCTTGTAAAGCATCACAAAGCATAGTGGTAGTTT 1501
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DB 1562 AGTAACCTGTGTGCATCTCTAGAGAGTGGGAAATAATGCTTGTACAAATTCGACCT 1621
QY 1621 AATATGTGCATTTGTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
DB 1622 AATATGTGCATTTGTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1681
QY 1681 ATGTTTTATTTACCTTTTGATATCTGTTGCAATGTTTAGTGATGTTTTAAAATGTGATG 1740
DB 1682 ATGTTTTATTTACCTTTTGATATCTGTTGCAATGTTTAGTGATGTTTTAAAATGTGATG 1741
QY 1741 AAAATATTAATGTTTTTAAGAGGAACAGTAGTGGAAATGAATGTTTAAAGATCTTTATGTG 1800
DB 1742 AAAATATTAATGTTTTTAAGAGGAACAGTAGTGGAAATGAATGTTTAAAGATCTTTATGTG 1801
QY 1801 TTTATGGTCTGCAGAGGATTTTTGTGATGAAGGGGATTTTTTGAAAAATTTAGAGAACT 1860
DB 1802 TTTATGGTCTGCAGAGGATTTTTGTGATGAAGGGGATTTTTTGAAAAATTTAGAGAACT 1861
QY 1861 AGCATATGGAATAATTAATGTTGTTTTTACCATGACTTTCAGTTCCTGTTTTTAGCTA 1920
DB 1862 AGCATATGGAATAATTAATGTTGTTTTTACCATGACTTTCAGTTCCTGTTTTTAGCTA 1921
QY 1921 GAACTTTAAACAAATAATAATAAGAAAAATAATAAGAGAGGAGGAGAGCAATG 1980
DB 1922 GAACTTTAAACAAATAATAATAAGAAAAATAATAAGAGAGGAGGAGCAATG 1981
QY 1981 TCTGATTCCTCTTTTGGTTTACCTGATTTCCATGATCATGCTTCTTCTGCAACACC 2040
DB 1982 TCTGATTCCTCTTTTGGTTTACCTGATTTCCATGATCATGCTTCTGCTGCAACACC 2041
QY 2041 CTCCTTAAGCAGCAGCAAGCAAGTGTGTCTGTACCATTTAGGAGTGTAGTAAAT 2100
DB 2042 CTCCTTAAGCAGCAGCAAGCAAGTGTGTCTGTACCATTTAGGAGTGTAGTAAAT 2101
QY 2101 AGTTGGCTAACTGCTCAAGTATTTTATACCCACAGAGAGGTATGTCACCTCATCTTACTTC 2160
DB 2102 AGTTGGCTAACTGCTCAAGTATTTTATACCCACAGAGAGGTATGTCACCTCATCTTACTTC 2161
QY 2161 CCAGGACATCCACCCTGAGAATAATTTGACAAGCTTAAAAATGGCTTCATGTGAGTGGC 2220
DB 2162 CCAGGACATCCACCCTGAGAATAATTTGACAAGCTTAAAAATGGCTTCATGTGAGTGGC 2221
QY 2221 AAAATTTGTTTTCTTCATTTAAATATTTTCTTGGCTAAATACATGTGAGAGGAGTAA 2280
DB 2222 AAAATTTGTTTTCTTCATTTAAATATTTTCTTGGCTAAATACATGTGAGAGGAGTAA 2281
QY 2281 ATATAATGTACAGAGGAAAGTTGAGTTCACCTCTGAAATGAGAATTTACTTGACAT 2340
DB 2282 ATATAATGTACAGAGGAAAGTTGAGTTCACCTCTGAAATGAGAATTTACTTGACAT 2341
QY 2341 TGGGATACCTTTAATCAGAAAAAAGAACTTATTTGAGCATTTTATCAACAAATTTTCATA 2400
DB 2342 TGGGATACCTTTAATCAGAAAAAAGAACTTATTTGAGCATTTTATCAACAAATTTTCATA 2401
QY 2401 ATTTGGACAATTTGAGGCAATTTATTTTAAAAACAATTTTATTTGGCTTTTGTCTAACAC 2460
DB 2402 ATTTGGACAATTTGAGGCAATTTATTTTAAAAACAATTTTATTTGGCTTTTGTCTAACAC 2461
QY 2461 AGTAAGCATGTATTTATTAAGGCATTCATTAATGCACACGCCCAAGCAATTAATTC 2520

Db 782 CGATCGGTGCAAGTGTAAAGAGTGAAGCCAACTTTGGCAAGCTATCTCAGCAAAAACATA 841
QY 841 CAGCTATGTTTATTCATGCCAAATATAAGCTCTGCAGAGAGTGGCTGCAATGAGGTCAAC 900
Db 842 CAGCTATGTTTATTCATGCCAAATATAAGCTGTGCAGAGAGTGGCTGCAATGAGGTCAAC 901
QY 901 AACGGTGGTGGATGTAAAGAGATCTTCAAGTCTCATCACCCATCCCTCGAACTCAAGT 960
Db 902 AACGGTGGTGGATGTAAAGAGATCTTCAAGTCTCATCACCCATCCCTCGAACTCAAGT 961
QY 961 CCGGCTCATTAACAAATCTTCTTGGCAGTGTCCACACATCTCTGCCCATCAAGATGTTCT 1020
Db 962 CCGGCTCATTAACAAATCTTCTTGGCAGTGTCCACACATCTCTGCCCATCAAGATGTTCT 1021
QY 1021 CATCATGTTCTTACGAGTGGCGTTCAGGATGATGCTTCTTGAATAATGCTTAGTTGAAAA 1080
Db 1022 CATCATGTTCTTACGAGTGGCGTTCAGGATGATGCTTCTTGAATAATGCTTAGTTGAAAA 1081
QY 1081 ATGGAGAGATCAGCTTAGTAAAGATCTCATACAGTGGGAAGAGAGGCTGCAGGAACAGCG 1140
Db 1082 ATGGAGAGATCAGCTTAGTAAAGATCTCATACAGTGGGAAGAGAGGCTGCAGGAACAGCG 1141
QY 1141 GAGACAGTTCAGGACAGCAAGAAACAGCCGGCGGCACCATCTGTAATCCGCCCAA 1200
Db 1142 GAGACAGTTCAGGACAGCAAGAAACAGCCGGCGGCACCATCTGTAATCCGCCCAA 1201
QY 1201 ACCAAGGAAAGCTCTGCTGCCAAACAGCCAGCTGCCAAGAGACATTTAAACTAG 1260
Db 1202 ACCAAGGAAAGCTCTGCTGCCAAACAGCCAGCTGCCAAGAGACATTTAAACTAG 1261
QY 1261 GAGTGGCCAGAGAGAACAAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG 1320
Db 1262 GAGTGGCCAGAGAGAACAAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG 1321
QY 1321 ACTTCGGAGTTCCTTACAGGATGAGGCTGGGCAATGCTGGGACAGCCCTATGTAAGGCCA 1380
Db 1322 ACTTCGGAGTTCCTTACAGGATGAGGCTGGGCAATGCTGGGACAGCCCTATGTAAGGCCA 1381
QY 1381 TGTGGCCCTTGGCCCTAACAACTCAGTGCAGTGTCTTCAATACAGACATCTTCGACGATTT 1440
Db 1382 TGTGGCCCTTGGCCCTAACAACTCAGTGCAGTGTCTTCAATACAGACATCTTCGACGATTT 1441
QY 1441 TTCTTAAGGCTATGCTTCAAGTCTTCTTTTGTAAAGCATCACAAAGCCATAGTGGTGGT 1500
Db 1442 TTCTTAAGGCTATGCTTCAAGTCTTCTTTTGTAAAGCATCACAAAGCCATAGTGGTGGT 1501
QY 1501 GCCCTTGTGACAGAGGTGAGCTTAAAGCTGGTGGAAAGGCTTATGCAATTCGATTCAG 1560
Db 1502 GCCCTTGTGACAGAGGTGAGCTTAAAGCTGGTGGAAAGGCTTATGCAATTCGATTCAG 1561
QY 1561 AGTAACCTGTGTCATCTTACAGAGTGAAGGAAATTAATGCTTGTACAAATTCGACCT 1620
Db 1562 AGTAACCTGTGTCATCTTACAGAGTGAAGGAAATTAATGCTTGTACAAATTCGACCT 1621
QY 1621 AATATGTCATTTGTAATAATGCAATATTTCAACAAACACGTAATTTTTTACAGT 1680
Db 1622 AATATGTCATTTGTAATAATGCAATATTTCAACAAACACGTAATTTTTTACAGT 1681
QY 1681 ATGTTTTATACCTTTGATATCTGTTGTGCAATGTTAGTATGTTTAAATGTGATG 1740
Db 1682 ATGTTTTATACCTTTGATATCTGTTGTGCAATGTTAGTATGTTTAAATGTGATG 1741
QY 1741 AAAATATATGTTTTTAAAGAGAACAGTGAAGTGAATGAATGTTTAAAGATCTTTATGTG 1800
Db 1742 AAAATATATGTTTTTAAAGAGAACAGTGAAGTGAATGAATGTTTAAAGATCTTTATGTG 1801
QY 1801 TTTATGGTCTCAGAGGATTTTTGTGATGAAAGGGGATTTTTTGAATAATTAGAGAACT 1860
Db 1802 TTTATGGTCTCAGAGGATTTTTGTGATGAAAGGGGATTTTTTGAATAATTAGAGAACT 1861
QY 1861 AGCATATGGAATAATATATGTTTTTTTACCAATGACTTCAGTTCTGTTTTTAGCTA 1920
Db 1862 AGCATATGGAATAATATATGTTTTTTTACCAATGACTTCAGTTCTGTTTTTAGCTA 1921

QY 1921 GAACTTAAAAACAAAAATAATAAAGAAAAATAAATAAAGAGAGAGGAGCAACAATG 1980
Db 1922 GAACTTAAAAACAAAAATAATAAAGAAAAATAAATAAAGAGAGAGGAGCAACAATG 1981
QY 1981 TCTGGATTCCTGTTTGGTTTACCTGATTTCCATGATCATGCTTCTTGTGCAACACC 2040
Db 1982 TCTGGATTCCTGTTTGGTTTACCTGATTTCCATGATCATGCTTCTTGTGCAACACC 2041
QY 2041 CTCTTAAGCAGCACCAGAAACAGTGTGCTGTACCATTTAGGAGTTTAGGTACTAAT 2100
Db 2042 CTCTTAAGCAGCACCAGAAACAGTGTGCTGTACCATTTAGGAGTTTAGGTACTAAT 2101
QY 2101 AGTTGGCTAATGCTCAAGTATTTATACCCACAAGAGAGTATGTCACCTCATCTTACTTC 2160
Db 2102 AGTTGGCTAATGCTCAAGTATTTATACCCACAAGAGAGTATGTCACCTCATCTTACTTC 2161
QY 2161 CCAGGACATCCACCCCTGAGATAATTTTGACAGCTTTAAAAATGGCCTTCATGTGAGTGGC 2220
Db 2162 CCAGGACATCCACCCCTGAGATAATTTTGACAGCTTTAAAAATGGCCTTCATGTGAGTGGC 2221
QY 2221 AAATTTGTTTCTTCTTCATTTAAATATTTTCTTGCCTAAATACATGTGAGAGGAGTTAA 2280
Db 2222 AAATTTGTTTCTTCTTCATTTAAATATTTTCTTGCCTAAATACATGTGAGAGGAGTTAA 2281
QY 2281 ATATAAATGTACAGAGAGGAAAGTTGAGTCCACCTCTCGAAATGAGAAATTTACTTTGACAGT 2340
Db 2282 ATATAAATGTACAGAGAGGAAAGTTGAGTCCACCTCTCGAAATGAGAAATTTACTTTGACAGT 2341
QY 2341 TGGGATACCTTTAATCAGAAAAAAGAACTTTTTCAGAGCTTTTATCAACAAATTTTCATA 2400
Db 2342 TGGGATACCTTTAATCAGAAAAAAGAACTTTTTCAGAGCTTTTATCAACAAATTTTCATA 2401
QY 2401 ATTGTGGCAATTTGGAGGCAATTTTAAAAAACAATTTTATGSCCTTTTGTCTAACAC 2460
Db 2402 ATTGTGGCAATTTGGAGGCAATTTTAAAAAACAATTTTATGSCCTTTTGTCTAACAC 2461
QY 2461 AGTAAGCATGTATTTTATAAGGCATTTCAATAATGACAAACGCCCAAGGAAATAAAATC 2520
Db 2462 AGTAAGCATGTATTTTATAAGGCATTTCAATAATGACAAACGCCCAAGGAAATAAAATC 2521
QY 2521 CTATCTAATCTCTACTCTCCACTACACAGAGGTAATCACTATTAGTATTTTGGCATATTTAT 2580
Db 2522 CTATCTAATCTCTACTCTCCACTACACAGAGGTAATCACTATTAGTATTTTGGCATATTTAT 2581
QY 2581 TCTCCAGGTGTTGCTTTATGCACTTATAAATGATTTGAACAAATAAAACTAGGAACCTG 2640
Db 2582 TCTCCAGGTGTTGCTTTATGCACTTATAAATGATTTGAACAAATAAAACTAGGAACCTG 2641
QY 2641 TATACATGTGTTTTCATAACCTGCCTCTTGTGCTTGGCCCTTTTATGAGATAAGTTTTCCT 2700
Db 2642 TATACATGTGTTTTCATAACCTGCCTCTTGTGCTTGGCCCTTTTATGAGATAAGTTTTCCT 2701
QY 2701 GTCAAGAAAGCAGAAACCATCTCATTTCTTACAGCTGTGTTTATATTTCCATAGTATGCAAT 2760
Db 2702 GTCAAGAAAGCAGAAACCATCTCATTTCTTACAGCTGTGTTTATATTTCCATAGTATGCAAT 2761
QY 2761 ACTCACAAACTGTTGCTGCTATTGGATACCTTAGGTGGTTTCTCACTGACAATACTGAAT 2820
Db 2762 ACTCACAAACTGTTGCTGCTATTGGATATTTGGATATTTAGGTGGTTTCTCACTGACAATACTGAAT 2821
QY 2821 AAACATCTCACCGGAATTC 2839
Db 2822 AAACATCTCACCGGAATTC 2840

RESULT 5

ABK92118

ID ABK92118 standard; DNA; 2820 BP.

XX ABK92118;

AC ABK92118;

XX 15-AUG-2002 (first entry)

XX DE Prostate cancer-associated DNA sequence #4.
XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX Mammalia.
XX OS WO200230268-A2.
XX PN 18-APR-2002.
XX PD 12-OCT-2001; 2001WO-US32045.
XX PF 13-OCT-2000; 2000US-0687576.
XX PR 08-DEC-2000; 2000US-0733288.
XX PR 08-DEC-2000; 2000US-0733742.
XX PR 24-JAN-2001; 2001US-263957P.
XX PR 16-MAR-2001; 2001US-276791P.
XX PR 16-MAR-2001; 2001US-276888P.
XX PR 06-APR-2001; 2001US-281922P.
XX PR 24-APR-2001; 2001US-286214P.
XX PR 30-APR-2001; 2001US-0847046.
XX PR 04-MAY-2001; 2001US-288589P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX P-PSDB; ABG61803.
XX WPI; 2002-471335/50.
XX DR
XX PT Detecting a prostate cancer-associated transcript in a cell in a
XX PT patient, useful for diagnosing prostate cancer (PC) or screening
XX PT modulators of PC, by determining if prostate cancer-associated genes
XX PT are expressed in a prostate tissue
XX PS Claim 22; Page 304; 436pp; English.
XX The present invention relates to methods of detecting a prostate
XX cancer-associated transcript in a cell from a patient. The method
XX comprises contacting a biological sample from the patient with
XX prostate cancer-associated polynucleotides (designated PC genes) that
XX selectively hybridise to a sequence that is at least 80% identical
XX to them. The prostate cancer-associated polynucleotide sequences
XX are differentially expressed in prostate tumour tissue or in
XX prostate cancer and are derived from the tissues of various
XX organisms such as humans or other mammals (e.g. mice, sheep and dogs).
XX The methods of the invention are useful for diagnosing and treating
XX prostate cancer in mammals. The prostate cancer-associated genes are
XX useful for diagnosing or treating prostate cancer, as well as for
XX identifying modulators of prostate cancer or agents that inhibit
XX prostate cancer. The nucleic acid sequences are particularly useful
XX in gene therapy, as a vaccine or in antisense applications.
XX ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
XX sequences.
XX SQ Sequence 2820 BP; 803 A; 619 C; 643 G; 755 T; 0 other;
Query Match 99.3%; Score 2820; DB 24; Length 2820;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 20 GCGCGGTTCCGCCCGGAGGCTGAGAGCTGGCGCTGCTGCGCTGCTGCTGCCAGCGG 79
DB 1 GCGCGGTTCCGCCCGGAGGCTGAGAGCTGGCGCTGCTGCGCTGCTGCTGCCAGCGG 60
OY 80 CGGAGCTCCGCCCGGAGGCTGAGAGCTGGCGCTGCTGCGCTGCTGCTGCCAGCGG 139
DB 61 CGGAGCTCCGCCCGGAGGCTGAGAGCTGGCGCTGCTGCGCTGCTGCTGCCAGCGG 120
OY 140 AAACCTCTCTCGGCCCGGAGGATTTCTTCTCGCGGAGGAGGACGCGGAGGATGAGGT 199
|||||

DB 121 AAACCTCTCTCGGCCCGGAGGATTTCTTCTCGCGGAGGAGACGCGAAAGATGAGGT 180
OY 200 GCGAGGAAAGAGAGCGCTTTCTGTCTGCGGGGTCGAGCGCGAGAGGCGAGTGCCATG 259
DB 181 GCGAGGAAAGAGAGCGCTTTCTGTCTGCGGGGTCGACGCGGAGAGGCGAGTGCCATG 240
OY 260 TTCTCTCCATCTAGTGGCGCTGTGGCTGTGGCTGTGCACCTGGCGCTGGCGCTGGCGGC 319
DB 241 TTCTCTCCATCTAGTGGCGCTGTGGCTGTGGCTGTGCACCTGGCGCTGGCGCTGGCGGC 300
OY 320 GCGCGCTCGGAGCGGTGGCATCTTATGTGCGCGGACATCCCTTGGAAACATCAGCGG 379
DB 301 GCGCGCTCGGAGCGGTGGCATCTTATGTGCGCGGACATCCCTTGGAAACATCAGCGG 360
OY 380 ATGCCCAACCACTGCACACAGCAGCAGGAGAGAGCGCATCTTGGCCATCAGCAGTAC 439
DB 361 ATGCCCAACCACTGCACACAGCAGCAGGAGAGAGCGCATCTTGGCCATCAGCAGTAC 420
OY 440 GAGGAGCTGGGAGCTGAACCTGACGCGCGTGTGGCTTCTTCTTGTGCCATGTATC 499
DB 421 GAGGAGCTGGGAGCTGAACCTGACGCGCGTGTGGCTTCTTCTTGTGCCATGTATC 480
OY 500 GCGCGCATTTGCACCTTGAGTTCTGTCACGACCTATCAAGCCGTCGAAGTCGGTGGC 559
DB 481 GCGCGCATTTGCACCTTGAGTTCTGTCACGACCTATCAAGCCGTCGAAGTCGGTGGC 540
OY 560 CAACGCGCGGCGGAGCTGCGAGCGCTCATGAAGATGTACAACACACAGCTGGCCGAA 619
DB 541 CAACGCGCGGCGGAGCTGCGAGCGCTCATGAAGATGTACAACACACAGCTGGCCGAA 600
OY 620 AGCCTGGCGCTGGAGAGCTGCTGTATGACCGTGGCGTGTGCATTTTCGCTGAAAGCC 679
DB 601 AGCCTGGCGCTGGAGAGCTGCTGTATGACCGTGGCGTGTGCATTTTCGCTGAAAGCC 660
OY 680 ATCGTCAGGAGCTCCCGGAGGATGTTAAGTGGATAGACATCACACGACATGATGTA 739
DB 661 ATCGTCAGGAGCTCCCGGAGGATGTTAAGTGGATAGACATCACACGACATGATGTA 720
OY 740 CAGGAAGCGCTTTGATGTTGACTGTAAACGCTTAAGCCGTCGCTGGTGAAGTGTAA 799
DB 721 CAGGAAGCGCTTTGATGTTGACTGTAAACGCTTAAGCCGTCGCTGGTGAAGTGTAA 780
OY 800 AAGGTGAAGCGCAACTTTGGCAACGATATCTCAGCAAAACCTACAGCTATGTTATTCATGCC 859
DB 781 AAGGTGAAGCGCAACTTTGGCAACGATATCTCAGCAAAACCTACAGCTATGTTATTCATGCC 840
OY 860 AAAATAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCAACCGGTGGTGAATGTAA 919
DB 841 AAAATAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCAACCGGTGGTGAATGTAA 900
OY 920 GAGATCTTCAAGTCTCATCACCCTCCCTGCAACTCAAGTCCCGCTCATTTACAATTC 979
DB 901 GAGATCTTCAAGTCTCATCACCCTCCCTGCAACTCAAGTCCCGCTCATTTACAATTC 960
OY 980 TCTTCCAGTGTCCACACATCTTGCCTGCAATCAAGATGTTCTCATCATGTTGTACGAGTG 1039
DB 961 TCTTCCAGTGTCCACACATCTTGCCTGCAATCAAGATGTTCTCATCATGTTGTACGAGTG 1020
OY 1040 CTTTCAAGATGATGCTTCTTGAATAATTTGCTTAGTTGAAAAATGGAGAGATCAGCTTACT 1099
DB 1021 CTTTCAAGATGATGCTTCTTGAATAATTTGCTTAGTTGAAAAATGGAGAGATCAGCTTACT 1080
OY 1100 AAAAGATCCATACAGTGGGAGAGAGGCTGCGAGGAACACGCGGAGACACGTTCCAGGACA 1159
DB 1081 AAAAGATCCATACAGTGGGAGAGAGGCTGCGAGGAACACGCGGAGACACGTTCCAGGACA 1140
OY 1160 AAGAAACAGCGCGGCGCACCACTGCTAGTAATCCCTCCCAACCAAGGAAAGCCTCCT 1219
DB 1141 AAGAAACAGCGCGGCGCACCACTGCTAGTAATCCCTCCCAACCAAGGAAAGCCTCCT 1200
OY 1220 GCTCCCAACAGCAGCTGCCAAGAGAACATTAACCTAGGAGTGCCCGAGAGAGACA 1279
DB 1201 GCTCCCAACAGCAGCTGCCAAGAGAACATTAACCTAGGAGTGCCCGAGAGAGACA 1260

QY 1280 AACCCGAAAAGAGTGTGAGCTAACTAGTTTCCAAAAGCGAGAGACTCCGACTTCCTTACAG 1339
 Db 1261 AACCCGAAAAGAGTGTGAGCTAACTAGTTTCCAAAAGCGAGAGACTCCGACTTCCTTACAG 1320
 QY 1340 GATGAGGCTGGGCATTTGCGTGGGACAGCCTATGTAAAGCCATGTGCCCTTCCCTTAACA 1399
 Db 1321 GATGAGGCTGGGCATTTGCGTGGGACAGCCTATGTAAAGCCATGTGCCCTTCCCTTAACA 1380
 QY 1400 ACTCACTGCAGTGCCTTCATAGACACATCTTGCAGCATTTTCTTAAGGCTATGCTTCA 1459
 Db 1381 ACTCACTGCAGTGCCTTCATAGACACATCTTGCAGCATTTTCTTAAGGCTATGCTTCA 1440
 QY 1460 GTTTTTCTTTTGAAGCCATCAACAAGCCATAGTGGTAGTTTGGCCCTTTGGGTACAGAAGGT 1519
 Db 1441 GTTTTTCTTTTGAAGCCATCAACAAGCCATAGTGGTAGTTTGGCCCTTTGGGTACAGAAGGT 1500
 QY 1520 GAGTTAAAGCTGGTGAAGGCTTATTCGATTCGATTCAGAGTAACCTGTGTCATGCT 1579
 Db 1501 GAGTTAAAGCTGGTGAAGGCTTATTCGATTCGATTCGAGTAACCTGTGTCATGCT 1560
 QY 1580 CTAGAAGAGTACGGGAAATTAATGCTTGTTCACAAATTCGACCTAATATGTCATTTGTAAT 1639
 Db 1561 CTAGAAGAGTACGGGAAATTAATGCTTGTTCACAAATTCGACCTAATATGTCATTTGTAAT 1620
 QY 1640 AAATGCCATATTTCAACAAAAACAGTAATTTTTTACAGTATGTTTTTATACCTTTTGA 1699
 Db 1621 AAATGCCATATTTCAACAAAAACAGTAATTTTTTACAGTATGTTTTTATACCTTTTGA 1680
 QY 1700 TATCTGTTGTCGAATGTTAGTGATGTTTTTAAAGTGTGATGAAAATATAATGTTTTTAAG 1759
 Db 1681 TATCTGTTGTCGAATGTTAGTGATGTTTTTAAAGTGTGATGAAAATATAATGTTTTTAAG 1740
 QY 1760 AAGGAACAGTACGTGAATCAATGTTTAAAGATCTTTATGTTTATGGTCTCAGAGGA 1819
 Db 1741 AAGGAACAGTACGTGAATCAATGTTTAAAGATCTTTATGTTTATGGTCTCAGAGGA 1800
 QY 1820 TTTTGTGTGTAAGGGGATTTTTTGAAAAATTAGAGAAGTAGCATATGGAAAAATATATA 1879
 Db 1801 TTTTGTGTGTAAGGGGATTTTTTGAAAAATTAGAGAAGTAGCATATGGAAAAATATATA 1860
 QY 1880 TGTGTTTTTTTACCAATGACTTCAGTTCTCTGTTTTTAGTAGTAACCTTAAAAACAATAAT 1939
 Db 1861 TGTGTTTTTTTACCAATGACTTCAGTTCTCTGTTTTTAGTAGTAACCTTAAAAACAATAAT 1920
 QY 1940 AATAAATAAGAAAAATAAATAAAGAGGAGGACAGCAATGCTGGATTCCTGTTTTTTG 1999
 Db 1921 AATAAATAAGAAAAATAAATAAAGAGGAGGACAGCAATGCTGGATTCCTGTTTTTTG 1980
 QY 2000 GTTACCTGATTTCCATGATCATGCTCTTGTGTCACACCCCTCTTAAGCAGCACCAGAA 2059
 Db 1981 GTTACCTGATTTCCATGATCATGCTCTTGTGTCACACCCCTCTTAAGCAGCACCAGAA 2040
 QY 2060 ACAGTGAGTTTGTCTGTACCATTTAGAGTTAGTACTAATAGTTGGCTAATGCTCAAGT 2119
 Db 2041 ACAGTGAGTTTGTCTGTACCATTTAGAGTTAGTACTAATAGTTGGCTAATGCTCAAGT 2100
 QY 2120 ATTTTATACCCACAGAGAGGTATGTCATCATCTTACTTCCAGGACATCCACCCTGAG 2179
 Db 2101 ATTTTATACCCACAGAGAGGTATGTCATCATCTTACTTCCAGGACATCCACCCTGAG 2160
 QY 2180 AATAATTTGACAAGCTTAAAAATGGCCTTCATGTGAGTGCCAAATTTGTTTTTCTTCAAT 2239
 Db 2161 AATAATTTGACAAGCTTAAAAATGGCCTTCATGTGAGTGCCAAATTTGTTTTTCTTCAAT 2220
 QY 2240 TTAATAATTTTCTTGGCCTTAAATACATGTGAGAGAGGTTAAATATAATGTACAGAGGG 2299
 Db 2221 TTAATAATTTTCTTGGCCTTAAATACATGTGAGAGAGGTTAAATATAATGTACAGAGGG 2280
 QY 2300 AAAGTTGAGTTCCACCTCTGAATGAGAATTAATCTGACAGTTGGGATCTTTAATCAGAA 2359
 Db 2281 AAAGTTGAGTTCCACCTCTGAATGAGAATTAATCTGACAGTTGGGATCTTTAATCAGAA 2340

QY 2360 AAAAAGAACTTTATTTGCAGCATTTTATCAACAAAATTTTCATAATTTGTGGACAAATTCGAGGC 2419
 Db 2341 AAAAAGAACTTTATTTGCAGCATTTTATCAACAAAATTTTCATAATTTGTGGACAAATTCGAGGC 2400
 QY 2420 ATTTATTTTAAAAACAATTTTATTTGGCCTTTTGTCTAACACAGTAAGCATGTATTTTATA 2479
 Db 2401 ATTTATTTTAAAAACAATTTTATTTGGCCTTTTGTCTAACACAGTAAGCATGTATTTTATA 2460
 QY 2480 AGGCATTTCAATTAATTCGACAAAGCCCAAGAGAAATAAAAATCCTATCTATCTACTCTCC 2539
 Db 2461 AGGCATTTCAATTAATTCGACAAAGCCCAAGAGAAATAAAAATCCTATCTACTCTCC 2520
 QY 2540 ACTACACAGAGTAATCACTATTAGTATTTTGGCATATTTATTTCTCCAGGTGTTTCTTAT 2599
 Db 2521 ACTACACAGAGTAATCACTATTAGTATTTTGGCATATTTATTTCTCCAGGTGTTTCTTAT 2580
 QY 2600 GCACCTTATAAATGATTTGCAACAATAAAGTAAGAACCTGTATACATGTGTTTCTATAAC 2659
 Db 2581 GCACCTTATAAATGATTTGCAACAATAAAGTAAGAACCTGTATACATGTGTTTCTATAAC 2640
 QY 2660 CTGCTCTCTTCTGCTGGCCCTTTTATTGAGATAAGTTTCTCTCAAGAAAGCAGAAACCA 2719
 Db 2641 CTGCTCTCTTCTGCTGGCCCTTTTATTGAGATAAGTTTCTCTCAAGAAAGCAGAAACCA 2700
 QY 2720 TCTCATTTCTTAACAGCTGTGTTTATATTCATATAGTATGCAATTAATCAACAAACTGTTGTGC 2779
 Db 2701 TCTCATTTCTTAACAGCTGTGTTTATATTCATATAGTATGCAATTAATCAACAAACTGTTGTGC 2760
 QY 2780 TATTGGATCTTATAGTGGTTTCTTCTCAGTCACAATGTAATAAATCTCACCAGGAAATTC 2839
 Db 2761 TATTGGATCTTATAGTGGTTTCTTCTCAGTCACAATGTAATAAATCTCACCAGGAAATTC 2820

RESULT 6

AAFP0598

ID AAFP0598 standard; cDNA; 2009 BP.

XX AAFP0598;

XX AC 08-JUN-2001 (first entry)

XX Receptor #86 partial coding sequence.

XX Probe; microarray; cancer; immunopathology; neuropathology; ss.

XX OS Homo sapiens.

XX PN US6183968-B1.

XX XX 06-FEB-2001.

XX PD 25-MAR-1999; 99US-0276531.

XX PF 27-MAR-1998; 98US-0079677.

XX PR (INCY-) INCYTE PHARM INC.

XX PI Bandman O, Lal P, Hillman JL, Yue H, Reddy R, Guegler KJ;

XX PI Baughm MR;

XX DR WPI; 2001-201999/20.

XX Composition having probes which comprise part of gene sequence encoding proteins associated with cell proliferation useful as hybridizable array elements in Microarrays to monitor expression of target polynucleotide -

PS Claim 1; Columns 167-170; 104pp; English.

XX The present invention relates to a composition comprising several polynucleotide probes. Probes can be derived from the present sequence. The probes are immobilised and are preferably useful as hybridisable array elements in a microarray for monitoring the expression of several

Db 1888 AAAATTAATGCTGCTTTTACAAATGACCTCAGCTCTGTTTTAGCTAGAACTCTAA 1947
Qy 1930 AAACAAAATAATAAAGAAAAATAATAAAGAGGAGGAGCAGACAA 1978
Db 1948 AAACAAAATAATAAAGAAAAATAATAAAGAGGAGGAGCAGAAAA 1996

RESULT 7
AAC84495
ID AAC84495 standard; DNA; 1767 BP.
XX AAC84495;
DT 02-APR-2001 (first entry)
XX Human FRAZZLED polypeptide encoding DNA.
XX FRAZZLED; antiinflammatory; osteopathic; immunosuppressive; AIDS;
XX antiarthritic; cerebroprotective; vasotropic; nephrotropic; antiHIV;
XX cyostatic; antiarteriosclerotic; nootropic; neuroprotective; vaccine;
XX gene therapy; human; ds.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 171..1211
CDS /*tag= a
FT /*product= "FRAZZLED polypeptide"
FT
XX

PN WO200075280-A2.
XX
XX 14-DEC-2000.
XX
XX 08-JUN-2000; 2000WO-US15814.
XX
XX 08-JUN-1999; 99US-0327869.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Lark MW, James IE, Kumar S;
XX
XX WPI; 2001-080596/09.
DR P-PSDB; AAB48183.
XX

PT New FRAZZLED polynucleotides and polypeptides useful for treating or
PT preventing e.g. acute and chronic inflammation, autoimmune disorders,
PT bone and cartilage diseases, cancers, or Alzheimer's disease
XX
XX Claim 2; Page 11; 37pp; English.
XX
XX The invention provides a human FRAZZLED polypeptide. The FRAZZLED
XX polynucleotides and polypeptides are useful for treating chronic and
XX acute inflammation (e.g. arthritis, osteoarthritis and other osteopenic
XX conditions), Paget's disease, septicemia, autoimmune diseases, infection,
XX stroke, ischemia, acute respiratory disease syndrome, renal disorders,
XX restenosis, brain injury, AIDS (acquired immunodeficiency syndrome),
XX metabolic and other bone diseases, cancer (e.g. bone and cartilage
XX cancers or tumors, lymphoproliferative disorders), atherosclerosis, and
XX Alzheimer's disease. The polynucleotides may be used as hybridization
XX probes for cDNA and genomic DNA, to isolate cDNA and genomic clones of
XX other genes having high sequence similarity to the FRAZZLED gene, and for
XX chromosome identification. The polypeptides may further be used as
XX immunogens to produce antibodies immunospecific for the FRAZZLED
XX polypeptides, as an immunological or vaccine formulation against the
XX above cited diseases, in screening for agonists and antagonists of the
XX FRAZZLED polypeptides, to configure assays for detecting the effect of
XX adding compounds on the production of FRAZZLED mRNA and protein in cells,
XX and to identify membrane bound or soluble ligand or receptors through
XX standard ligand/receptor binding techniques. The present sequence
XX represents the DNA encoding the human FRAZZLED polypeptide.
XX
XX Sequence 1767 BP; 468 A; 432 C; 456 G; 411 T; 0 other;

Query Match	60.1%;	Score 1706.2;	DB 22;	Length 1767;
Best Local Similarity	99.3%;	Pred. No. 0;		
Matches 1755;	Conservative 0;	Mismatches 8;	Indels 4;	Gaps 4;
Qy 88	CGCGCGCGACCCCGCGCGCGCTTTGCTGCGGACTGGAGTTTGGGGAAGAAACTCTC	147		
Db 1	CGCGCGCGACCCCGCGCGCGCTTTGCTGCGGACTGGAGTTTGGGGAAGAAACTCTC	60		
Qy 148	CTGCGCCCCAGAAAGATTTCCTCGGCGAAGGGACACGAAAGATGAGGTTGGCAGAA	207		
Db 61	CTGCGCCCCAGAGGATTTCCTCGGCGAAGGGACACGAAAGATGAGGTTGGCAGAA	120		
Qy 208	GAGAA-GGCGGCTTCTGCTGCGCGGGTTCGACGCGGAGAGGCGAGTGCCTCTCT	266		
Db 121	GAGAAAGGCGGCTTCTGCTGCGCGGGTTCGACGCGGAGAGGCGAGTGCCTCTCT	180		
Qy 267	CCATCTAGTGGCGCTGTGCTGCGCTGCGCTGCGCTGCGCTGCGCGCGCGCTCT	326		
Db 181	CCATCTAGTGGCGCTGTGCTGCGCTGCGCTGCGCTGCGCTGCGCGCGCGCTCT	240		
Qy 327	CGGAGGCGGTGCGCATCCCTATGTGCCGCGACATCCCTGGAACATCAGCGGATGCCA	386		
Db 241	CGGAGGCGGTGCGCATCCCTATGTGCCGCGACATCCCTGGAACATCAGCGGATGCCA	300		
Qy 387	ACCACCTGCACACACGACGAGGAGAACGCCATCCTGCGCATCGAGCAGTACGAGGAC	446		
Db 301	ACCACCTGCACACACGACGAGGAGAACGCCATCCTGCGCATCGAGCAGTACGAGGAC	360		
Qy 447	TGGTGGACGTGAACGTGACGCGCGTGTGCGCTTCTTCTGCTGCCATGTACGCGGCA	506		
Db 361	TGGTGGACGTGAACGTGACGCGCGTGTGCGCTTCTTCTGCTGCCATGTACGCGGCA	420		
Qy 507	TTTGACCCCTGGAGTTCTGTCGACGACCCATCAACCGCTGCAAGTCTGCAACCGG	566		
Db 421	TTTGACCCCTGGAGTTCTGTCGACGACCCATCAACCGCTGCAAGTCTGCAACCGG	480		
Qy 567	CGCGGACGACTGCGAGCCCTCATGAAGATGTACAACACACAGCTGGCCGAAAGCCCTGG	626		
Db 481	CGCGGACGACTGCGAGCCCTCATGAAGATGTACAACACACAGCTGGCCGAAAGCCCTGG	540		
Qy 627	CCTGCGAGCGTGCCTGTCTATGACCGTGGGTGTGATTTTGGCTGAAAGCATCGTCA	686		
Db 541	CCTGCGAGCGTGCCTGTCTATGACCGTGGGTGTGATTTTGGCTGAAAGCATCGTCA	600		
Qy 687	CGGACCTCCGAGGATCTTAAGTGGATAGACATCACACACACATGATGGTACAGGAA	746		
Db 601	CGGACCTCCGAGGATCTTAAGTGGATAGACATCACACACACATGATGGTACAGGAA	660		
Qy 747	GGCCTCTTTGATTTGACTGTAAACGCCCTAAGCCCGCATCGGTGCAAGTGTAAAAAGTGA	806		
Db 661	GGCCTCTTTGATTTGACTGTAAACGCCCTAAGCCCGCATCGGTGCAAGTGTAAAAAGTGA	720		
Qy 807	AGCCAACTTTGGCAACGATCTCAGCAAAAACATACAGCATGTATTATTCATGCCAAAATAA	866		
Db 721	AGCCAACTTTGGCAACATATCTCAGCAAAAACATACAGCATGTATTATTCATGCCAAAATAA	780		
Qy 867	AAGCTGTCGACGAGTGGCTGCAATGAGTTCACACCGGTGGTGCATGTAAAGAGATCT	926		
Db 781	AAGCTGTCGACGAGTGGCTGCAATGAGTTCACACCGGTGGTGCATGTAAAGAGATCT	840		
Qy 927	TCAAGTCTCATACCCCATCCCTCGAACTCAAGTCCCGCTCATTTACAAATTTCTTCTTGGC	986		
Db 841	TCAAGTCTCATACCCCATCCCTCGAACTCAAGTCCCGCTCATTTACAAATTTCTTCTTGGC	900		
Qy 987	AGTGTCCACACATCTGCCCATCAAGATGTTCTCATCATGTGTGTACGAGTGGCGTTCAA	1046		
Db 901	AGTGTCCACACATCTGCCCATCAAGATGTTCTCATCATGTGTGTGTACGAGTGGCGTTCAA	960		
Qy 1047	GGATGATGCTTCTGAAAATTCGCTTAGTTGAAAATGCAGAGATCAGCTTAGTAAAGAT	1106		
Db 961	GGATGATGCTTCTTGAATAATTCGCTTAGTTGAAAATGCAGAGATCAGCTTAGTAAAGAT	1020		

QY 387 ACCACCTGACACACAGCAGCAGAGAGAACGCCATCCTTGCCCATCGAGCAGTACGAGGAGC 446
Db 301 ACCACCTGACACACAGCAGCAGAGAGAACGCCATCCTTGCCCATCGAGCAGTACGAGGAGG 360
QY 447 TGGTGGAGCTGAACCTGACAGCGCGTGTGCGCTTCTTCTTGTCGCCATGACGCGCCA 506
Db 361 TGGTGGAGCTGAACCTGACAGCGCGTGTGCGCTTCTTCTTGTCGCCATGACGCGCCA 420
QY 507 TTTTGACCTGGAGTTCCTGACAGCAGCCTATCAAGCGGTGCAAGTCGGTGTGCCAACGGG 566
Db 421 TTTTGACCTGGAGTTCCTGACAGCAGCCTATCAAGCGGTGCAAGTCGGTGTGCCAACGGG 480
QY 567 CGCGGAGCAGCTCGAGCGCCCTCATGAAGATGTACAACACACAGCTGGCCCGAAAGCCTGG 626
Db 481 CGCGGAGCAGCTCGAGCGCCCTCATGAAGATGTACAACACACAGCTGGCCCGAAAGCCTGG 540
QY 627 CTTGGAGCAGCTGCTGTCTATGACCGTGGCGTGTGATTTTCGGCTGAAGCCATCGTCA 686
Db 541 CTTGGAGCAGCTGCTGTCTATGACCGTGGCGTGTGATTTTCGGCTGAAGCCATCGTCA 600
QY 687 CGGACCTCCCGAGGATGTTAAGTGGATAGACATCACACCAGACATGATGTTACAGGAAA 746
Db 601 CGGACCTCCCGAGGATGTTAAGTGGATAGACATCACACCAGACATGATGTTACAGGAAA 660
QY 747 GGCCTCTTGATGTTGACTGTAAACGCCCTAAGCCCGATCGGTGCAAGTGTAAAGAGTGA 806
Db 661 GGCCTCTTGATGTTGACTGTAAACGCCCTAAGCCCGATCGGTGCAAGTGTAAAGAGTGA 720
QY 807 AGCCAACTTTGGCAAGTATCTCAGCAAAAACCTAGACGATGTTATTCATGCGCAAAATAA 866
Db 721 AGCCAACTTTGGCAAGTATCTCAGCAAAAACCTAGACGATGTTATTCATGCGCAAAATAA 780
QY 867 AAGCTGTGCAGAGAGTGGCTGCAATGAGTGCACACCGTGTGATGTTAAAGAGATCT 926
Db 781 AAGCTGTGCAGAGAGTGGCTGCAATGAGTGCACACCGTGTGATGTTAAAGAGATCT 840
QY 927 TCAAGTCTCTCATACCCATCCCTCGAACTCAAGTCCGCTCATTACAAATTTCTTTGCC 986
Db 841 TCAAGTCTCTCATACCCATCCCTCGAACTCAAGTCCGCTCATTACAAATTTCTTTGCC 900
QY 987 AGTGTCCACACATCTGCCCCATCAAGATGTTCTCATGTTTACAGTGGCGTTCA 1046
Db 901 AGTGTCCACACATCTGCCCCATCAAGATGTTCTCATGTTTACAGTGGCGCTCAA 960
QY 1047 GGATGATGCTTCTTGAATAATTCCTTAGTTGAAATAATGGAGATCAGCTTAGTAAAGAT 1106
Db 961 GGATGATGCTTCTTGAATAATTCCTTAGTTGAAATAATGGAGATCAGCTTAGTAAAGAT 1020
QY 1107 CCATACAGTGGAGAGAGGCTGCGAGAACACGCGGAGAACAGTTTCAGGACACAGAAAA 1166
Db 1021 CCATACAGTGGAGAGAGGCTGCGAGAACACGCGGAGAACAGTTTCAGGACACAGAAAA 1080
QY 1167 CAGCGCGGCGCACAGTGTGTAGTATCCCGCAACCAAGGGAAGCTTCTGCTCCA 1226
Db 1081 CAGCGCGGCGCACAGTGTGTAGTATCCCGCAACCAAGGGAAGCTTCTGCTCCA 1140
QY 1227 AACACAGCAGTCCCAAGAGAACATTTAAAACTAGGAGTGCCCGAGAGAACAAACCGCA 1286
Db 1141 AACACAGCAGTCCCAAGAGAACATTTAAAACTAGGAGTGCCCGAGAGAACAAACCGCA 1200
QY 1287 AAAGAGTGTAGCTAACTAGTTTCCAAAGCGGAGACTTCCGACTTCTTACAGGATGAGG 1346
Db 1201 AAAGAGTGTAGCTAACTAGTTTCCAAAGCGGAGACTTCCGACTTCTTACAGGATGAGG 1260
QY 1347 CTGGGCATTCCTGGACAGCCTATGTAAAGCCATGTCGCCCTTCCCTAACAACCTACT 1406
Db 1261 CTGGGCATTCCTGGACAGCCTATGTAAAGCCATGTCGCCCTTCCCTAACAACCTACT 1320
QY 1407 CGAGTGTCTTCATAGACACATCTTGCAGCATTTTCTTAAGCTATGCTTCAGTTTTC 1466
Db 1321 CGAGTGTCTTCATAGACACATCTTGCAGCATTTTCTTAAGCTATGCTTCAGTTTTC 1380

QY 1467 TTTTGAAGCCATCACAGCCATAGTGGTAGGTTTGCCTTTTGGTACAGAAAGTGAGTTAA 1526
Db 1381 TTTTGAAGCCATCACAGCCATAGTGGTAGGTTTGCCTTTTGGTACAGAAAGTGAGTTAA 1440
QY 1527 ACCTGGTGGAAAAGCTTATTCGATTTCAGATTTCAGAGTAACCTGTGTCATCTCTAGAAG 1586
Db 1441 ACCTGGTGGAAAAGCTTATTCGATTTCGATTTCAGAGTAACCTGTGTCATCTCTAGAAG 1500
QY 1587 AGTAGGAAAAATTAATGCTTGTTCACAAATTCGACCTAATATGTGCATTGTAATAAATGCC 1646
Db 1501 AGTAGGAAAAATTAATGCTTGTTCACAAATTCGACCTAATATGTGCATTGTAATAAATGCC 1560
QY 1647 ATATTTCAACAAAAACACGTAATTTTTCACAGTAGTATGTTTTTATACCTTTTGTATCTGT 1706
Db 1561 ATATTTCAACAAAAACACGTAATTTTTCACAGTAGTATGTTTTTATACCTTTTGTATCTGT 1620
QY 1707 TGTTCGAATGTTAGTGTGATGTTTAAATGCTGAT-GAATAATATATGTTTTTAAG-AAGCA 1764
Db 1621 TGTTCGAATGTTAGTGTGATGTTTAAATGCTGATGTAATAATATATGTTTTTAAGAAAGGA 1680
QY 1765 ACAGTAGTGGAAATGAATGT-TAAAAAGATCTTTTATGTTTATGTTGCTGCAGAAAGATTTT 1823
Db 1681 ACAGTAGTGGAAATGAATGTCTAAAGATCTTTTATGTTTATGTTGCTGCAGAAAGATTTT 1740
QY 1824 TGTGATGAAAGGGATTTTTTGAAGAA 1850
Db 1741 TGTGATGAAAGGGATTTTTTGAAGAA 1767

.. RESULT 9
AAV80658
ID AAV80658 standard; cDNA; 1969 BP.
XX AC AAV80658;
XX DF 15-MAR-1999 (first entry)
XX DE Partial human FRAZZLED protein encoding cDNA.
KW Human; FRAZZLED protein; PR2B; chronic inflammation; acute inflammation;
KW arthritis; osteoarthritis; septicemia; autoimmune disease; cancer;
KW transplant rejection; graft versus host disease; infection; stroke;
KW ischaemia; acute respiratory disease syndrome; renal disorder;
KW restenosis; brain injury; AIDS; cancer; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 200..1318
FT /*tag= .a
FT /product= "partial frazzled protein"
FT /transl_except= (pos:254..256,aa:Xaa)
FT /note= "Xaa is unspecified"
XX XX
PN EP887406-A2.
XX XX
PD 30-DEC-1998.
XX XX
PF 23-APR-1998; 98EP-0303163.
XX XX
PR 26-NOV-1997; 97US-0978981.
PR 22-MAY-1997; 97US-0047408.
XX XX
PA (SMK) SMITHKLINE BEECHAM CORP.
XX XX
PI James I, Kumar S, Lark M;
XX XX
DR WPI; 1999-047873/05.
XX XX
PT P-PSDB; AAV86347.
XX XX
PT New FR2B-related (FRAZZLED) polypeptide and polynucleotide - useful
PT as diagnostic reagents and for prevention and treatment of cancer,
PT Alzheimer's disease and AIDS

XX PS Example 1; Page 9-10; 25pp; English.

CC The present sequence encodes partial human FRAZZLED protein from the

CC FR2B family. The FR2B family controls signalling and developmental

CC patterning. FRAZZLED proteins and polynucleotides are useful for

CC diagnosing diseases related to over or underexpression of FRAZZLED

CC protein by identifying mutations in the FRAZZLED gene, or determining

CC FRAZZLED protein expression levels. FRAZZLED proteins can be used to

CC screen for agonists and antagonists which bind the FRAZZLED protein

CC by observing the binding, or stimulation or inhibition of FRAZZLED

CC activity. These can be used in treatment to activate (agonist) or

CC inhibit (antagonist) FRAZZLED activity, in addition to direct

CC administration of antisense sequences to prevent expression, or FRAZZLED

CC polynucleotides to treat conditions associated with a lack of FRAZZLED

CC protein. Gene therapy may also be used to affect endogenous FRAZZLED

CC protein production. FRAZZLED antibodies are useful for inducing an

CC immune response to immunise and prevent diseases, and for isolating

CC FRAZZLED clones or purifying the protein by affinity chromatography.

CC FRAZZLED proteins can be administered directly or as a vaccine to

CC inoculate against diseases. Diseases diagnosed, prevented or treated

CC include: chronic and acute inflammation, arthritis, osteoarthritis,

CC septicemia, autoimmune diseases, transplant rejection, graft versus

CC host disease, infection, stroke, ischaemia, acute respiratory disease

CC syndrome, renal disorders, restenosis, brain injury, AIDS and cancer.

XX SQ Sequence 1969 BP; 504 A; 484 C; 518 G; 458 T; 5 other:

Query Match 59.7%; Score 1694.8; DB 20; Length 1969;

Best Local Similarity 96.4%; Pred. No. 0;

Matches 1854; Conservative 0; Mismatches 49; Indels 21; Gaps 11;

Qy 14 TTCTAGGCGGGTTCGCCGCCCGAGGCTGAGAGTGGCGTGTCTGCGCCCTGTGTGCC 73

Db 22 TGCCCGGGCGGGTTCGCCGCCCGAGGCTGAGAGTGGCGTGTCTGCGCCCTGTGTGCC 81

Qy 74 AGACGGCGAGCTCGCGGGCGGAGCCCGCGGCCGCTTTTGTGCGGACGTGGATTTGG 133

Db 82 AGACGGCGAGCTCGCGGGCGGAGCCCGCGGCCGCTTTTGTGCGGACGTGGATTTGG 141

Qy 134 GGGAGAAATCTCTCGCGGCCCGAGAGATTTCTTCGCGGAGGAGGACGCGAAGAT 193

Db 142 GGGAGAAATCTCTCGCGGCCCGAGAGATTTCTTCGCGGAGGAGGACGCGAAGAT 201

Qy 194 GAGGTGCGAGGAGAGAA-GCGCGTTTCTGCTGCGCGGGGTGCGAGCGGAGGGGAG 252

Db 202 GAGGTGCGAGGAGAGAGGGCGCTTCTGCTGCGCGGGGTGCGAGCGGAGGGGAG 261

Qy 253 TGCCATGTTCTCTCCATCTCTAGTGGGCTGTGCGTGTGGGTG-CACCTGCGCGTGGCG 311

Db 262 TGCCATGTTCTCTCCATCTCTAGTGGGCTGTGCGTGTGGGTG-CACCTGCGCGTGGCG 321

Qy 312 TG-CGCGCGCGCCCTCGGAGG-CGGTGGCATCCCTATGTGCGGGGCACATGCCCTGGAA 369

Db 322 TGTGCGCGCGCCCTCGAGAGGTGGTGGCATCCCTATGTGCGGGGCACATGCCCTGGAA 381

Qy 370 CATCACGGGATGCCCAACACCTGCACACAGCAGCAGGAGAACGCCATCTCGGCCAT 429

Db 382 CATCACGGGATGCCCAACACCTGCACACAGCAGCAGGAGAACGCCATCTCGGCCAT 441

Qy 430 CGAGCAGTACGAGGAGCTGGTGGAGCTGGAAGTGCAGCGCCGCTGTGCGCTTCTTCTG 489

Db 442 CGAGCAGTACGAGGAGCTGGTGGAGCTGGAAGTGCAGCGCCGCTGTGCGCTTCTTCTG 501

Qy 490 TGCCATGTACGCGGCCATTTGCACCTGGAGTTCTGACAGCCCTATCAAGCGGTGCAA 549

Db 502 TGCCATGTACGCGGCCATTTGCACCTGGAGTTCTGACAGCCCTATCAAGCGGTGCAA 561

Qy 550 GTCGCTGTCGAACGCGCGGAGCTGCGAGCCCTCATGAGATGTACAACACAG 609

Db 562 GTCGCTGTCGAACGCGCGGAGCTGCGAGCCCTCATGAGATGTACAACACAG 621

Qy 610 CTGCCCCGAAAGCCTGGCCTGCGAGAGCTGCCTGTCTATCACCGTGGCGTGCATTTTC 669

Db 622 CTGCCCCGAAAGCCTGGCCTCGAGAGCTGCCTCTCTATGACCGTGGCGTGCATCTC 681

Qy 670 GCCTGAAGCCATCTGTCAGGACCTCCCGAGAGTGTAAAGTGGATAGACATCACACCAGA 729

Db 682 GCCTGAAGCCATCTGTCAGGACCTCCCGAGAGTGTAAAGTGGATAGACATCACACCAGA 741

Qy 730 CATGATGTTACAGGAAGGCCCTCTTGTGTTGACTGTAAAGCCCTAAAGCCCGATCGGTG 789

Db 742 CATGATGTTACAGGAAGGCCCTCTTGTGTTGACTGTAAAGCCCTAAAGCCCGATCGGTG 801

Qy 790 CAAGTGTAAAGGTGAAGCCAACTTTGGCAACGTATCTCAGCAAAACTACAGTATGT 849

Db 802 CAAGTGTAAAGGTGAAGCCAACTTTGGCAACATATCTCAGCAAAACTACAGTATGT 861

Qy 850 TATTTCATGCCAAATAAAGCTGTGCAGAGGTTGGCTGCAATGAGTGCACAACGGTGT 909

Db 862 TATTTCATGCCAAATAAAGCTGTGCAGAGGTTGGCTGCAATGAGTGCACAACGGTGT 921

Qy 910 GGATGTAAAGAGATCTTCAAGTCTCATCAACCCATCCCTCGAATCAAGTCCCGCTCAT 969

Db 922 GGATGTAAAGAGATCTTCAAGTCTCATCAACCCATCCCTCGAATCAAGTCCCGCTCAT 981

Qy 970 TACAAATTTCTTCTGCGAGTGTCCACATCTGCCCCCATCAAGATGTTCTCATGTGTG 1029

Db 982 TACAAATTTCTTCTGCGAGTGTCCACATCTGCCCCCATCAAGATGTTCTCATGTGTG 1041

Qy 1030 TTACGAGTGGGCTTCAAGGATGATGCTTCTTGAAATTTGCTTAGTGTGAAATGAGAGA 1089

Db 1042 TTACGAGTGGGCTTCAAGGATGATGCTTCTTGAAATTTGCTTAGTGTGAAATGAGAGA 1101

Qy 1090 TCAGCTTAGTAAAGATCCATACAGTGGGAAGAGAGGCTGCAGGAACCGGAGAACAGT 1149

Db 1102 TCAGCTTAGTAAAGATCCATACAGTGGGAAGAGAGGCTGCAGGAACCGGAGAACAGT 1161

Qy 1150 TCAGGACAAGAAAGAACAGCGCGGCGCACAGTGTAGTATATCCCGCCCAACCAAGGG 1209

Db 1162 TCAGGACAAGAAAGAACAGCGCGGCGCACAGTGTAGTATATCCCGCCCAACCAAGGG 1221

Qy 1210 AAAGCTCTCTCTCCCAACAGCCAGTCCCAAGGAAGAACATTAACACTAGGAGT- ---- 1264

Db 1222 AAAGCTCTCTCTCCCAACAGCCAGTCCCAAGGAAGAACATTAACACTAGGAGTTCGACC 1281

Qy 1265 ----GCCCCAGAGAGAACAAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG 1320

Db 1282 CACGGCTCCGAGAGAGAACAAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG 1341

Qy 1321 ACTTCCGACTTCTTACAGGATGAGGCTGGGCTGGGACAGCCCTATGTAAGGCCA 1380

Db 1342 ACTTCCGACTTCTTACAGGATGAGGCTGGGCTGGGACAGCCCTATGTAAGGCCA 1401

Qy 1381 TGTGCCCCCTGCGCTTAACAACCTCACTGCAGTGCCTTCTATAGACACATCTTGCAGCATTT 1440

Db 1402 TGTGCCCCCTGCGCTTAACAACCTCACTGCAGTGCCTTCTATAGACACATCTTGCAGCATTT 1461

Qy 1441 TTCTTAAGGCTATGCTTCAAGTCTTCTTGTAAAGCCATCAAGCCATAGTGGTGGTGT 1500

Db 1462 TTCTTAAGGCTATGCTTCAAGTCTTCTTGTAAAGCCATCAAGCCATAGTGGTGGTGT 1521

Qy 1501 GCCCTTTGGTACAGAGGTGAGTTAAAGCTGGTGGAAAGGCTTATTCGATTTGCATTCAG 1560

Db 1522 GCCCTTTGGTACAGAGGTGAGTTAAAGCTGGTGGAAAGGCTTATTCGATTTGCATTCAG 1581

Qy 1561 AGTAACTGTGTGATATCTTAGAAGAGTAGGGAATAATGCTTGTACAATTCGACCT 1620

Db 1582 AGTAACTGTGTGATATCTTAGAAGAGTAGGGAATAATGCTTGTACAATTCGACCT 1641

Qy 1621 AATATGTCATTTGTAATAAATGCTATTTTCAACAAAAACACCTAATATTTTTTACAGT 1680

Db 1642 AATATGTCATTTGTAATAAATGCTATTTTCAACAAAAACACCTAATATTTTTTACAGT 1701

Qy 1681 ATGTTTTATTACCTTTTGTATCTGTTGCAATGTTAGTGTGATGTTTTTAAATGTGATG 1740

Qy	850	TATTTCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGTGCACAACGGTGGT	909
Db	862	TATTTCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGTGCACAACGGTGGT	921
Qy	910	GGATGTAAAGAGATCTTCAAGTCCCTCATACCCATCCCTCGAACTCAAGTCCCGCTCAT	969
Db	922	GGATGTAAAGAGATCTTCAAGTCCCTCATACCCATCCCTCGAACTCAAGTCCCGCTCAT	981
Qy	970	TACAAATCTTCTTGCCAGTGTCCACACATCTGCCCCATCAAGATGTTCTTCATCATGTG	1029
Db	982	TACAAATCTTCTTGCCAGTGTCCACACATCTGCCCCATCAAGATGTTCTTCATCATGTG	1041
Qy	1030	TTACGAGTGGCGTTCAAGGATGATGCTTCTTGAAATTTGCTTACTTGAAAAATGGAGAGA	1089
Db	1042	TTACGAGTGGCGTTCAAGGATGATGCTTCTTGAAATTTGCTTACTTGAAAAATGGAGAGA	1101
Qy	1090	TCAGCTTAGTMAAGATCCATACAGTGGGAGAGAGAGCTGCAGGAACAGCGGAGACAGT	1149
Db	1102	TCAGCTTAGTMAAGATCCATACAGTGGGAGAGAGAGCTGCAGGAACAGCGGAGACAGT	1161
Qy	1150	TCAGGACAAGAGAAACAGCGGGCGCACCATGCTAGTAATCCCCCAAAACCAAAAGG	1209
Db	1162	TCAGGACAAGAGAAACAGCGGGCGCACCATGCTAGTAATCCCCCAAAACCAAAAGG	1221
Qy	1210	AAAGCCTCTGCTGCCAAACACAGCCAGCTGCCAAGAGAACAATTAAACTAGGAGT-----	1264
Db	1222	AAAGCCTCTGCTGCCAAACACAGCCAGCTGCCAAGAGAACAATTAAACTAGGAGT-----	1281
Qy	1265	----GCCAGAGAGAAACAAACCCGAAAGAGTGTGAGCTAACTAGTTCCTCAAAAGCGGAG	1320
Db	1282	CAGCGGTGCCAGAGAAACAAACCCGAAAGAGTGTGAGCTAACTAGTTCCTCAAAAGCGGAG	1341
Qy	1321	ACTTCGCACTTCTTACAGGATGAGGCTGGGCATTGGCTGGGACAGCCTATGTAAAGSCCA	1380
Db	1342	ACTTCGCACTTCTTACAGGATGAGGCTGGGCATTGGCTGGGACAGCCTATGTAAAGSCCA	1401
Qy	1381	TGTGCCCTTGGCCTAACCACTCACTGCAAGTGCCTTCATAGACACATCTTGCAAGCATTT	1440
Db	1402	TGTGCCCTTGGCCTAACCACTCACTGCAAGTGCCTTCATAGACACATCTTGCAAGCATTT	1461
Qy	1441	TTCTTAAGGCTATGCTTCAGTTTTCTTTTGTAAAGCCATCACAAGCCATAGTGGTAGGTTT	1500
Db	1462	TTCTTAAGGCTATGCTTCAGTTTTCTTTTGTAAAGCCATCACAAGCCATAGTGGTAGGTTT	1521
Qy	1501	GCCTTTTGGTACAGAAGGTGAGTTAAAGCTGGTGAAAGGCTTTATGTCATTCGATTCAG	1560
Db	1522	GCCTTTTGGTACAGAAGGTGAGTTAAAGCTGGTGAAAGGCTTTATGTCATTCGATTCAG	1581
Qy	1561	AGTAACCTGTGTCATCTACTAGAAAGTGTAGGAAATTAATGCTTGTACAATTCGACCT	1620
Db	1582	AGTAACCTGTGTCATCTACTAGAAAGTGTAGGAAATTAATGCTTGTACAATTCGACCT	1641
Qy	1621	AAATATGTCATTTGTAATTAATGTCATTTTCAACAAAAACAGTAAATTTTTTTACAGT	1680
Db	1642	AAATATGTCATTTGTAATTAATGTCATTTTCAACAAAAACAGTAAATTTTTTTACAGT	1701
Qy	1681	ATGTTTTATTACCTTTTGATATCTGTTGTGCAATGTTAGTGATGTTTAAATGTGATG	1740
Db	1702	ATG-TTTATTACCTTTTGATATCTGTTGTGCAATGTTAGTGATGTTTAAATGTGATG	1760
Qy	1741	AAAATATAATGTTTTTAAAGAGAACAGTAGT-GGAATGAATGT-TAAAAGATCTTTTATG	1798
Db	1761	AAAATATAATGTTTTTAAAGAGAACAGTAGTGGGAATGAATGCTTAAAGATCTTTTATG	1820
Qy	1799	TGTTTTATGGTCTG-CAGAAAGATTTTTTGTATGAAGGGGATTTTTTGAAGAAA--TTAGA	1855
Db	1821	TGTTTTATGGTCTGCCAAGAGGATTTTTTGTATGAAGGGGATTTTTTGAAGAAAATCTAGG	1880
Qy	1856	GAAGTAGC--ATATGCAAAATTAATGTGTTTTTTTACCATGACATTCAGTTCTCTGTTT	1913
Db	1881	GAGTAGCCATATGGGAAATTAATNATGTGCTTTTTTACATGACATTCAGGCTCCGTTT	1940
Qy	1914	TTAG 1917	

Db 1941 111 TTTG 1944

RESULT 11

ABQ88234
ID ABQ88234 standard: cDNA: 1969 BP.

AA ABQ88234;

18-SEP-2002 (first entry)

XX DE Human osteoblast differentiation related cDNA SEQ ID NO 141.

AA Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW osteoporosis; osteopathic; ss.

XX Homo sapiens.

XX PN WO200250301-A2

XX
PD
27-JUN-2002.

18-DEC-2001: 2001WO-US48276.

PR 18-DEC-2000: 2000US-255882P.

PR 24-APR-2001; 2001US-285691P.
XX

PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE

XX Ji D. Axelrod DW. Cook JS.
PI

PI Mertz L;
XX

DR
XX
WFL; 2002-55/663/59.

PT Use of genes and the
PT differentiation for

PT or treating e.g. osteoporosis, or as markers for the differentiation process -
PT
XX
PS Claim 1; SEQ ID NO 141; 78pp + Sequence Listing; English.

CC The invention relates to genes and their expression profiles

CC (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition;
CC (b) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition;

(c) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporosis; or
 (d) treating or monitoring treatment of the conditions cited in (b).

CC monitoring the progression of bone tissue deposition.

CC Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteopenia, osteodys trophy

CC drug-induced abnormalities in bone formation or bone loss, conditions
CC that involve altered bone metabolism (e.g. idiopathic juvenile
CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis
CC osteoneogenesis

CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC osteoblast differentiation associated cDNA marker of the invention.

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1969 BP; 504 A; 484 C; 518 G; 458 T; 5 other;

Best Local Similarity 96.4%; Pred. NO. 0;
Matches 1854; Conservative 0; Mismatches 49; Indels 21; Gaps 1

QY 14 TTCTAGGGGGGTTTCGCGCCCGCGCTGAGAGCTGGCGCTGCTCGTGCCTGTGTGCC 73

DD ZZ TGCCCGGCGGGGTTCGCACCCCCCAAGGCCCTGAAGAATCAGCACCTCATGTTT

.

QY /4 AGACGGCGGAGCTCCGCGGGCCGGACCCCCGCGGCGCTTTGCTGCTCCGACTGGAGTTTGG 133

Query Match	59.7%	Score 1694.8;	DB 24;	Length 1969;
Best Local Similarity	96.4%;	Pred. NO. 0;		
Matches 1854;	Conservative	0;	Mismatches 49;	Indels 21; Gaps 11;

QV 14 TTCTAGGGCGGGGTTTCGGCGCCCCCGAAGGCTGAGAGCTGGCGCTGCTCGTGCCCTGTGTGCC 73

db 22 TGCCCGGGGGTTCCGGCCCCGAAGGCTGAGAGCTGGCGCTGCTCGTGCCTGTGTGCC 81

74 AGACGGCGGAGCTCCGCGGCGGACCCCGCGGCCCCGCTTTGCTGCCGACTGGAGTTTGG 133

Db 82 AGACGGCGAGCTCGCGCGCGGACCCCGCGGCCCGCTTTGCTGCCACATGGAGTTGG 141
Qy 134 GGAAGAAACTCTCTCTGCGGCCGAGAAATTTCTTCCTCGGGAAGGACACAGCGAAAGAT 193
Db 142 GGAAGAAACTCTCTCTGCGGCCGAGAGATTTCTTCCTCGGGAAGGACACAGCGAAAGAT 201
Qy 194 GAGGTGGCAGGAAGAGAA - GCGCGTTCTTCTGTCTGCGCGGGTTCGAGCGCGAGAGGCGAG 252
Db 202 GAGGTGGCAGGAAGAGGCGCTTCTGTCTGCGCGGGTTCGAGCGCGAGANGCGAG 261
Qy 253 TGCCATGTTCTCTCTCATCTAGTGGCGCTGTGCGCTGTGGCTG - CACCTGGGCGTGGCGG 311
Db 262 TGCCATGTTCTCTCATCTAGTGGCGCTGTGCGCTGTGGCTGTACCTGGGCGTGGCGG 321
Qy 312 TG - CCGCGCGCGCCCTGCGAGG - CGGTGCGCATCCCTATGTGCGCGGCACATGCCCTGGAA 369
Db 322 TGTCGCGCGCGCCCTGAGCAGGTGCGGTGGCATCCCTATGTGCGCGGCACATGCCCTGGAA 381
Qy 370 CATCACGCGGATGCCCAACCACTGCACACAGCAGCAGGAGAACGCCATCTCGGCCAT 429
Db 382 CATCACGCGGATGCCCAACCACTGCACACAGCAGCAGGAGAACGCCATCTCGGCCAT 441
Qy 430 CGAGCAGTACGAGGAGCTGTGGAGCTGAACTGCAGCGCGCTGTGCGGTCTTCTCTG 489
Db 442 CGAGCAGTACGAGGAGCTGTGGAGCTGAACTGCAGCGCGCTGTGCGGTCTTCTCTG 501
Qy 490 TGCCATGTACGCGCGCCATTTGACCCCTGGAGTTCTGTGACGACCCCTATCAAGCCGTGAA 549
Db 502 TGCCATGTACGCGCGCCATTTGACCCCTGGAGTTCTGTGACGACCCCTATCAAGCCGTGAA 561
Qy 550 GTGCGTGTGCCAACCGCGCGGAGCTGCGAGCCCTCATGAAGATGTACAACACAG 609
Db 562 GTGCGTGTGCCAACCGCGCGGAGCTGCGAGCCCTCATGAAGATGTACAACACAG 621
Qy 610 CTGGCGCGGAAAGCCCTGGCGAGAGCTGCTGTATGACCCGTGGCGTGTGATTTTC 669
Db 622 CTGGCGCGGAAAGCCCTGGCGAGAGCTGCTGTATGACCCGTGGCGTGTGATTTTC 681
Qy 670 GCCTGAAGCCATCTGTCAGGAGCTCCCGGAGGATGTTAAGTGGATAGACATCACACCAGA 729
Db 682 GCCTGAAGCCATCTGTCAGGAGCTCCCGGAGGATGTTAAGTGGATAGACATCACACCAGA 741
Qy 730 CATGATGTACAGGAAGCCCTCTTGATGTTGACTGTAAACGCCCTAAGCCCCGATCGGTG 789
Db 742 CATGATGTACAGGAAGCCCTCTTGATGTTGACTGTAAACGCCCTAAGCCCCGATCGGTG 801
Qy 790 CAAGTGTAAAGAGTGAAGCCAACTTTGGCACAGTATCTCACCAAAACTACAGCTATGT 849
Db 802 CAAGTGTAAAGAGTGAAGCCAACTTTGGCAACATATCTCACCAAAACTACAGCTATGT 861
Qy 850 TATTCATGCAAAATAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAAACGCTGT 909
Db 862 TATTCATGCAAAATAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAAACGCTGT 921
Qy 910 GGATGTAAAGAGATCTTCAAGTCTCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCAT 969
Db 922 GGATGTAAAGAGATCTTCAAGTCTCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCAT 981
Qy 970 TACAATAATCTTCTGCGAGTGTGCACACATCTGCGCCCATCAAGATGTTCTCATATGTG 1029
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Qy 1030 TTACGAGTGGCTTCAAGGATGATCTTCTTGAATAATGCTTAGTTGAATAATGGAGAGA 1089
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Qy 1090 TCAGCTTAGTAAAGATCCATACAGTGGGAAGAGAGGCTGCGAGAACACGCGGAGAACAGT 1149
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Qy 1150 TCAGGCAAGAGAAACACGCGCGGCGGACCATGCTAGTAAATCCCGCCCAACCAAGG 1209
|||||

Db 1162 TCAGGCAAGAGAAACACAGCGCGGCGGACCATGCTAGTAAATCCCGCCCAACCAAGGG 1221
Qy 1210 AAAGCTCTCTCTCCCAAAACAGCAGCTCCCAAGAAAGCAATTAATACTAGGAGT - ---- 1264
Db 1222 AAAGACTCTCTCTCCCAAAACAGCAGCTCCCAAGAAAGCAATTAATACTAGGCGTCCAGC 1281
Qy 1265 ---GCCCAAGAGAGAAACCCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG 1320
Db 1282 CACGCGTCCGAAGAGAAACCCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG 1341
Qy 1321 ACTTCCGACTCTCTTACAGGATGAGCTGGCATTTCCCTGGGACAGCCTATGTGAAGGCCA 1380
Db 1342 ACTTCCGACTCTCTTACAGGATGAGCTGGCATTTCCCTGGGACAGCCTATGTGAAGGCCA 1401
Qy 1381 TGTGCCCCCTTGGCCCTAACAACCTCACTGCAGTGTCTTTCATAGACACATCTTTCACAGATTT 1440
Db 1402 TGTGCCCCCTTGGCCCTAACAACCTCACTGCAGTGTCTTTCATAGACACATCTTTCACAGATTT 1461
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Db 1522 GCCCTTTTGTACAGAGGTGAGTTAAAGCTGCTGGAAGAGGCTTATGCAATTTGCAATTCAG 1581
Qy 1561 AGTAACCTCTGTGCATCTCTAGAGAGTAGGGAATAAATGCTTTGTACAAATTCGACCT 1620
Db 1582 AGTAACCTCTGTGCATCTCTAGAGAGTAGGGAATAAATGCTTTGTACAAATTCGACCT 1641
Qy 1621 AATATGTCATGTTAAATAAATGATGATTTTCAACAAACAAACACAGTAAATTTTTTACAGT 1680
Db 1642 AATATGTCATGTTAAATAAATGATGATTTTCAACAAACAAACACAGTAAATTTTTTACAGT 1701
Qy 1681 ATGTTTTTATACCTTTTGTATATCTGTTGCAATGTTAGTGTATGTTTAAATGTTGATG 1740
Db 1702 ATG - TTTATATACCTTTTGTATATCTGTTGCAATGTTAGTGTATGTTTAAATGTTGATG 1760
Qy 1741 AAAATATAATGTTTAAAGAGGAACAGTAGT - GGAATGAATGT - TAAAGATCTTTATG 1798
Db 1761 AAAATATAATGTTTAAAGAGGAACAGTAGTGGGAATGAATGCTCTTAAAGATCTTTATG 1820
Qy 1799 TGTTTATGTCGTG - CAGAAGGATTTTGTGATGAAGGGGATTTTGTGAAAAA - TTAGA 1855
Db 1821 TGTTTATGTCGTGCGCAGAGGATTTTGTGATGAAGGGGATTTTGTGAAAAA - TTAGG 1880
Qy 1856 GAAGTAGC - ATATGGAATAATATAATGTTTGTGTTTACCAATGACTTTCAGTTTCTGTTT 1913
Db 1881 GAAGTAGCCATATGGGAAAAATATATATGTTGCTCTTTTACATGGAGTCCAGTCCGTTT 1940
Qy 1914 TTAG 1917
Db 1941 TTTG 1944
RESULT 12
AAAX28656
ID AAX28656 standard; cDNA; 1581 BP.
XX
AC AAX28656;
XX
DT 16-AUG-1999 (first entry)
XX
DE Full length clone encoding the human frezzled-like protein.
XX
KW Human frezzled-like protein; HFLP; frezzled protein family;
KW differentiation-related disorder; agonist; antagonist; antibody;
KW haematopoiesis; wound healing; cancer; inflammatory disorder;
KW autoimmune disease; allergic reaction; ss.
OS Homo sapiens.
FH Key Location/Qualifiers

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FT CDS 78...1184
FT /*tag= a
FT /product= "human frezzled-like protein"
FT sig_peptide 78...206
FT /*tag= b
FT mat_peptide 206...1181
FT /*tag= c
FT
XX
PN W09909152-A1.
XX
PD 25-FEB-1999.
XX
PF 11-AUG-1998; 98WO-US16701.
XX
PR 10-APR-1998; 98US-0081438.
PR 12-AUG-1997; 97US-0055715.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen HS, Ruben SM;
XX
XX WPI; 1999-190159/16.
DR P-PSDB; AAY03232.
XX
XX New isolated human frezzled-like protein - used to develop products
PT for treating e.g. cancers, inflammatory and autoimmune diseases,
PT infectious diseases and allergic reactions
XX
XX Disclosure; Fig 2A-2B; 152pp; English.
XX
CC This is the nucleotide sequence of the full length clone encoding
CC the human frezzled-like protein (HFLP), used in the method of the
CC invention. It is a member of the frizzled protein family. It is
CC used in the detection and treatment of differentiation-related
CC disorders. In conditions where HFLP is under-expressed, its agonist
CC is involved in the treatment. Antagonist and antibodies of HFLP are
CC used in the treatment of disorder where HFLP is over-expressed, e.g.
CC the regulation of haematopoiesis, and wound healing. HFLP products
CC are used to develop products for treating e.g. cancers, inflammatory
CC and autoimmune diseases, infectious diseases and allergic
CC reactions.
XX
SQ Sequence 1581 BP; 415 A; 412 C; 405 G; 345 T; 4 other;
Query Match 54.3%; Score 1541.2; DB 20; Length 1581;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1560; Conservative 2; Mismatches 17; Indels 1; Gaps 1;
1
QY 115 GCTGCCGACTGAGTTTGGGGGAGAAACTCTCTCGCGCCCGCAGAGATTCTTCTCTCGG 174
DB 1 GCTGCCGACTGAGTTTGGGGGAGAAACTCTCTCGCGCCCGCAGAGATTCTTCTCTCGG 60
QY 175 CGAAGGACAGCGAAGATGAGGTGGCAGGAGAGAA- GCGGCTTCTGCTGCGCGGGG 233
DB 61 CGAAGGACAGCGAAGATGAGGTGGCAGGAGAGAGAGGGCGCTTCTGCTGCGCGGGG 120
QY 234 TCGCAGCGCGAGAGGCGAGTGCATGTTCTCTCCATCTCTAGTGGCGTGTGCTGTGGC 293
DB 121 TCGCAGCGCGAGAGGCGAGTGCATGTTCTCTCCATCTCTAGTGGCGTGTGCTGTGGC 180
QY 294 TGCACCTGGCGTGGCGTGGCGGCGCGCGCTGCGAGCGGTGCGCATTCCTATGTGCC 353
DB 181 TGCACCTGGCGTGGCGTGGCGGCGCGCGCTGCGAGCGGTGCGCATTCCTATGTGCC 240
QY 354 GGCACATGCCCTGGACATCAGCGGATGCCCAACCACTGCAACACGACGCGAGGAGA 413
DB 241 GGCACATGCCCTGGACATCAGCGGATGCCCAACCACTGCAACACGACGCGAGGAGA 300
QY 414 AGCCATCTCTGGCCATCGAGAGTACGAGAGCTGTGTGGACGTGAACTCGACGCGGTGC 473
DB 301 AGCCATCTCTGGCCATCGAGAGTACGAGAGCTGTGTGGACGTGAACTCGACGCGGTGC 360
QY 474 TGGCTTCTTCTTCTGTGCCATGTACGCGGCCCATTTGCAACCTGGAGTTCTCTGCAGGC 533
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DB 361 TGGCTTCTTCTTCTGTGCCATGTACGGGCCCATTTGCAACCTGGAGTTCCTGCGAGCC 420
QY 534 CTATCAAGCGGTGCAAGTCTGGTGTGCCAACGCGCGGAGCGACTGCGAGCCCTCATGA 593
DB 421 CTATCAAGCGGTGCAAGTCTGGTGTGCCAACGCGCGGAGCGACTGCGAGCCCTCATGA 480
QY 594 AGATGTACAACACACAGCTGGCCCGAAAGCCTGGCCCTGGGAGAGTGGCTGTCTATGACC 653
DB 481 AGATGTACAACACACAGCTGGCCCGAAAGCCTGGCCCTGGGAGAGTGGCTGTCTATGACC 540
QY 654 GTGGCGTGTGCATTTCCGCTGAGGCCATCTGCACGAGCTCCCGGAGAGATGTTAAGTGA 713
DB 541 GTGGCGTGTGCATCTCGCTGAAAGCATCTGCACGAGCTCCCGGAGAGTGTAAAGTGA 600
QY 714 TAGACATCACACACACATGATGTACAGAAAGCCCTCTTGTATGTTGACTGTAAAGCCG 773
DB 601 TAGACATCACACACACATGATGTACAGAAAGCCCTCTTGTATGTTGACTGTAAAGCCG 660
QY 774 TAAGCCCGGATCGGTGCAAGTGTAAAGAGTGAAGCCCAACTTTGGCAAGTATCTCAGCA 833
DB 661 TAAGCCCGGATCGGTGCAAGTGTAAAGAGTGAAGCCCAACTTTGGCAACATATCTCAGCA 720
QY 834 AAACTACAGCTATGTTTATTCATGCGCAAAATAAAAGCTGTGCAGAGAGTGGCTGCAATG 893
DB 721 AAACTACAGCTATGTTTATTCATGCGCAAAATAAAAGCTGTGCAGAGAGTGGCTGCAATG 780
QY 894 AGGTCACAACGCGTGGTGGATGTAAAGAGATCTTCAAGTCCCTCATCACCCTCCGAA 953
DB 781 AGGTCACAACGCGTGGTGGATGTAAAGAGATCTTCAAGTCCCTCATCACCCTCCGAA 840
QY 954 CTCAGTCCCGCTCATTAACAATTTCTTGTGCAAGTGTCCACACATCTCTGCCCATCAAG 1013
DB 841 CTCAGTCCCGCTCATTAACAATTTCTTGTGCAAGTGTCCACACATCTCTGCCCATCAAG 900
QY 1014 ATGTTCTCATCATGTTTACGAGTGGGTTCGAGTATGATGTTCTTGAATAATTCGTTAG 1073
DB 901 ATGTTCTCATCATGTTTACGAGTGGGTTCGAGTATGATGTTCTTGAATAATTCGTTAG 960
QY 1074 TTGAAATATGGAGACATCAGCTTACTTAAAGATCCATACAGTGGGAGAGAGCTGCAGG 1133
DB 961 TTGAAATATGGAGACATCAGCTTACTTAAAGATCCATACAGTGGGAGAGAGCTGCAGG 1020
QY 1134 AACAGCGGAGAACAGTCTCAGGACAAAGAAACAGCGCGGCGCACCATCTAGTAGTAATC 1193
DB 1021 AACAGCGGAGAACAGTCTCAGGACAAAGAAACAGCGCGGCGCACCATCTAGTAGTAATC 1080
QY 1194 CCCCCAAACCAAGGAAAGCCTCTGCTCCCAACAGCAGCAGTCCCAAGAGAACATTA 1253
DB 1081 CCCCCAAACCAAGGAAAGAGTCTCTGCTCCCAACAGCAGTCCCAAGAGAACATTA 1140
QY 1254 AAACCTAGGAGTCCCGCAGAGAGAACAAACCCGAAAGAGTGTAGCTAACTAGTTCCAA 1313
DB 1141 AAACCTAGGAGTCCCGCAGAGAGAACAAACCCGAAAGAGTGTAGCTAACTAGTTCCAA 1200
QY 1314 AGCGGAGACTTCCGACTTCTTACAGGATGAGGCTGGGCAATTCCTGGGACAGCCTATGT 1373
DB 1201 AGCGGAGACTTCCGACTTCTTACAGGATGAGGCTGGGCAATTCCTGGGACAGCCTATGT 1260
QY 1374 AAGGCGATGTGCCCTTGGCCCTTAAACATCACTGCGATGCTCTTCATAGACACATCTTCG 1433
DB 1261 AAGGCGATGTGCCCTTGGCCCTTAAACATCACTGCGATGCTCTTCATAGACACATCTTCG 1320
QY 1434 AGCATTTTCTTAAAGCTATGCTTCAAGTCTTCTTGTAAAGCCATCACAGCCATAGTGG 1493
DB 1321 AGCATTTTCTTAAAGCTATGCTTCAAGTCTTCTTGTAAAGCCATCACAGCCATAGTGG 1380
QY 1494 TAGGTTTGGCCCTTGGTACAGAGGTGAGCTTAAAGCTGTGGAAAGGCTTATTGCATTG 1553
DB 1381 TAGGTTTGGCCCTTGGTACAGAGGTGAGCTTAAAGCTGTGGAAAGGCTTATTGCATTG 1440
QY 1554 CATTCAGAGTAACTGTGTGCATACCTCTAGAGAGTAGGAGAAATAATGCTTGTTCATAAT 1613
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Db 1441 CATTCAAGTAACCTGTGTGCATACCTCTASAAAGTAGGAGAAATAATGCTTGTACAAAT 1500
 QY 1614 TCGACCTAATATGTGCATTGTAAATAAATGACATATTTCAACAAAACACAGCTAATTTT 1673
 Db 1501 TCTACCTAATATGTGCATTGTATAAATAATGACATATTTCAACAAAACACAGCTAATTTT 1560
 QY 1674 TTACAGTATGTTTTATTACC 1693
 Db 1561 TTACAGTATGCTCACTACC 1580

RESULT 13
 AAZ33454
 ID AAZ33454 standard; cDNA; 1556 BP.
 XX
 AC AAZ33454;
 XX
 DT 08-DEC-1999 (first entry)
 XX
 DE Human prostate cancer-associated EST 32.
 XX
 KW Expressed sequence tag; EST; prostate tumor; antitumor; treatment;
 KW gene therapy; tissue specificity human; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19811193-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 10-MAR-1998; 98DE-1011193.
 XX
 PR 10-MAR-1998; 98DE-1011193.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 XX
 DR WPI; 1999-519628/44.
 DR P-PSDB; AAY48252.
 XX
 PT New nucleic acid expressed at high level in prostatic tumor tissue and
 PT encoded polypeptides, useful for treating cancer and screening for
 PT therapeutic agents .
 PS
 PS Claim 3; 94; 166pp; German.
 XX
 CC This invention describes novel nucleic acid sequences (A) that are
 CC expressed at high level in prostatic tumor tissue and encode gene
 CC products or their fragments. The products of the invention have
 CC antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for
 CC identifying agents for treatment of prostatic cancer and (ii) for
 CC therapy of prostate cancer, optionally where expressed by gene therapy
 CC methods. (A) is also used to isolate full-length genes (for gene therapy
 CC and for recombinant production of (I), which can be used to raise
 CC specific antibodies. (A) are identified by assembly of ESTs (expressed
 CC sequence tags) before they are analyzed for expression pattern (tissue
 CC specificity). This approach eliminates many of the false results, as
 CC regards tissue specificity, associated with known methods that use
 CC single (usually short) ESTs. AAZ33454-233476 represent expressed
 CC sequence tags described in the method of the invention.
 XX
 SQ Sequence 1556 BP; 479 A; 330 C; 363 G; 384 T; 0 other;

Query Match 50.4%; Score 1432; DB 20; Length 1556;
 Best Local Similarity 97.8%; Pred. No. 5.3e-300;
 Matches 1494; Conservative 0; Mismatches 30; Indels 4; Gaps 4;

QY 455 GTGAAGTGCAGCGCGTGTGGC-TTCTTCTCTGTGCGATGACGCGCCCATTTGGAC 513
 Db 1 GTGAAGTGCAGCGCGTGTGGC-TTCTTCTCTGTGCGATGACGCGCCCATTTGGAC 60

QY 514 CTTGAGTTCCTGCAGCAACCTATCAAGCGGTGCAAGTGTGCGCAACGCGCGCGCA 573

Db 61 CCTGGAGTTCTCGCAGACCTTATCAAGCGTGCAGTGGTGTGCAACGCGCGCA 120
 QY 574 CCACCTGCGAGCGCTCATGAAGATGTACACACAGCTGGCGCGAAGCTGGCTGCA 633
 Db 121 CCACCTGCGAGCGCTCATGAAGATGTACACACAGCTGGCGCGAAGCTGGCTGCA 180
 QY 634 CGAGCTGCTGTCTATGACCGTGGCGTGTGCATTTTCGCTGAAGCATCTGTCAGGACCT 693
 Db 181 CGAGCTGCTGTCTATGACCGTGGCGTGTGCATCTGCTGAAGCATCTGTCAGGACCT 240
 QY 694 CCCGAGGATGTTAAGTGGATAGACATCACACAGACATGATGGTACAGAAAGGCTCT 753
 Db 241 CCCGAGGATGTTAAGTGGATAGACATCACACAGACATGATGGTACAGAAAGGCTCT 300
 QY 754 TGATGTTGACTGTAAACGCTTAAGCCCGATCGGTGCAAGTGTAAAGAGTGAAGCCAAC 813
 Db 301 TGATGTTGACTGTAAACGCTTAAGCCCGATCGGTGCAAGTGTAAAGAGTGAAGCCAAC 360
 QY 814 TTTGGCAACGTATCTCAGCAAAACTACAGCTATGTTATTTCATGCCAAATAAAGCTCT 873
 Db 361 TTTGGCAACGTATCTCAGCAAAACTACAGCTATGTTATTTCATGCCAAATAAAGCTCT 420
 QY 874 GCAGAGGATGCTGCAATGAGGTCAACAGGTGGTGGATGTAAAGAGATCTTCAAGTC 933
 Db 421 GCAGAGGATGCTGCAATGAGGTCAACAGGTGGTGGATGTAAAGAGATCTTCAAGTC 480
 QY 934 CTCATCACCCTATCCCTCGAAGTCAAGTCCCGCTCATACAAATTTCTTTCGCAAGTCT 993
 Db 481 CTCATCACCCTATCCCTCGAAGTCAAGTCCCGCTCATACAAATTTCTTTCGCAAGTCT 540
 QY 994 ACACATCTCTGCCCATCAAGATGTTCTCATCATGTGTACAGTGGCTTCAAGGATGAT 1053
 Db 541 ACACATCTCTGCCCATCAAGATGTTCTCATCATGTGTACAGTGGCTTCAAGGATGAT 600
 QY 1054 GCTTCTTCAAAATGCTTAGTTGAAAAATGGAGATCAGCTTAGTAAAGATCCATACA 1113
 Db 601 GCTTCTTCAAAATGCTTAGTTGAAAAATGGAGATCAGCTTAGTAAAGATCCATACA 660
 QY 1114 GTGGGAAGAGCGCTGCAGGAACAGCGGAGACAGTTTCAGGACAGAGAAACAGCGCG 1173
 Db 661 GTGGGAAGAGCGCTGCAGGAACAGCGGAGACAGTTTCAGGACAGAGAAACAGCGCG 720
 QY 1174 GCGCACCGTCTAGTAAATCCCGCAACAAAGGAAAGCGCTCTGCTCCCAACAGCAG 1233
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 QY 1234 CAGTCCCAGAGAAACATTTAAACTAGGAGTCCCGCAGAGAGAGAAACACCCGAAAGAT 1293
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 QY 1294 GTGAGCTAAGTATGTTCCAAACGCGAGAGCTTCCGACTTCTTACAGGATGAGGCTGGGA 1353
 Db 841 GTGAGCTAAGTATGTTCCAAACGCGAGAGCTTCCGACTTCTTACAGGATGAGGCTGGGA 900
 QY 1354 TTGCGCTGGCAGACCTATGTAAGGCGATGTCGCCCTTGAACAACTCACTGCGAGTGC 1413
 Db 901 TTGCGCTGGCAGACCTATGTAAGGCGATGTCGCCCTTGAACAACTCACTGCGAGTGC 960
 QY 1414 TCTTCATAGACACATCTTGCAGCATTTTCTTAAGGCTATGCTTCAGTTTCTTTTGTAA 1473
 Db 961 TCTTCATAGACACATCTTGCAGCATTTTCTTAAGGCTATGCTTCAGTTTCTTTTGTAA 1020
 QY 1474 GCCATCAGAGCCATAGTGGTAGGTTTGGCCCTTTCGTACAGAGGAGTGAAGCTGCT 1533
 Db 1021 GCCATCAGAGCCATAGTGGTAGGTTTGGCCCTTTCGTACAGAGGAGTGAAGCTGCT 1080
 QY 1534 GGAAAGGCTTATTCGATTGCAATTCAGAGTAACCTGTGTGCATCTCTAGAAGAGTAGG 1593
 Db 1081 GGAAAGGCTTATTCGATTGCAATTCAGAGTAACCTGTGTGCATCTCTAGAAGAGTAGG 1140
 QY 1594 AAAATAATGCTTGTACAACTTCGACCTAATATGTCATTTGTAATAAATAATGTCATATTC 1653

Db 742 GATGGTACAGGAAGCCCTTCTGATGTTGACTGTAAACGCCTAAGCCCGATCGGTGCAA 801
QY 793 GTCTAAAAAGGTGAAGCCCACTTTGGCAACGTATCTCAGCAAAAACTACAGCTATGTTAT 852
Db 802 GTCTAAAAAGGTGAAGCCCACTTTGGCAACGTATCTCAGCAAAAACTACAGCTATGTTAT 861
QY 853 TCATGCCAAATAAAGCTGTGTCAGAGGAGTGGCTGCAATGAGGTGCACACGGTGTGGA 912
Db 862 TCATGCCAAATAAAGCTGTGTCAGAGGAGTGGCTGCAATGAGGTGCACACGGTGTGGA 921
QY 913 TGTAAAGAGATCTTCAAGTCTCATCACCCATCCCTGCAACTCAAGTCCCGCTCATTTAC 972
Db 922 TGTAAAGAGATCTTCAAGTCTCATCACCCATCCCTGCAACTCAAGTCCCGCTCATTTAC 981
QY 973 AAATCTCTTGGCAGTGTCCACACATCTCTGCCCATCAAGATGTTCTCATCATGTGTTA 1032
Db 982 AAATCTCTTGGCAGTGTCCACACATCTCTGCCCATCAAGATGTTCTCATCATGTGTTA 1041
QY 1033 CGAGTGGCTTCAAGGATGATGTTCTTGAATTTGCTTAGTTTGAATAATGGAGATCA 1092
b 1042 CGAGTGGCTTCAAGGATGATGTTCTTGAATTTGCTTAGTTTGAATAATGGAGATCA 1101
QY 1093 GCTTACTAAAGATCCTACAGTGGGAGAGAGGCTGCAGGAACACGGGAGACAGTTCA 1152
Db 1102 GCTTACTAAAGATCCTACAGTGGGAGAGAGGCTGCAGGAACACGGGAGACAGTTCA 1161
QY 1153 GGACAAGAAACAGCGGGCCACCACTGCTAGTAAATCCCTCCCAACCAAGGAA 1212
Db 1162 GGACAAGAAACAGCGGGCCACCACTGCTAGTAAATCCCTCCCAACCAAGGAA 1221
QY 1213 GCCTCTGTCTCCCAACCAAGAGTGTCCCAAGAGACATTTAAACTAGGAGTGGCCAGAA 1272
Db 1222 GCCTCTGTCTCCCAACCAAGAGTGTCCCAAGAGACATTTAAACTAGGAGTGGCCAGAA 1281
QY 1273 GACAACAAACCCCAAGAGTGTGAGCTACTAGTTTCCAAAGCGGAGACTTCGACTTC 1332
Db 1282 GAACAACAAACCCCAAGAGTGTGAGCTACTAGTTTCCAAAGCGGAGACTTCGACTTC 1341
QY 1333 CTTACAGGATGAGGCTGGGATTCCTTGGGACAGCTATGTAAAGCCATGTGCCCCCTTC 1392
Db 1342 CTTACAGGATGAGGCTGGGATTCCTTGGGACAGCTATGTAAAGCCATGTGCCCCCTTC 1401
QY 1393 CTTAACAATCACTGAGTGGCTC-TTCATAGACACATCTTGGAGCATTTTCTTAA 1447
Db 1402 CTTAACAATCTCCCTGAGTGGCTCTTCTCATAGACACATCTTGGAGCATTTTCTTAA 1457

RESULT 15
ABQ54454
ID ABQ54454 standard; cDNA; 1216 BP.

XX AC ABQ54454;

XX DT 22-AUG-2002 (first entry)

XX DE Human ovarian antigen HNOKB73 cDNA, SEQ ID NO:334.

XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.

XX OS Homo sapiens.

XX SS WO200200677-A1.

PN PN 03-JAN-2002.

PD

XX PF 07-JUN-2001; 2001WO-US18569.
XX PR 07-JUN-2000; 2000US-209467P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI: 2002-147878/19.
XX DR P-PSDB; ABP41377.
XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX PT useful in the prevention, treatment and diagnosis of cancer (e.g.
XX PT ovarian cancer), immune disorders, cardiovascular disorders and
XX PT neurological diseases -
XX PS Claim 1: SEQ ID NO 334; 2922pp; English.
XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents cDNA encoding a human ovarian antigen of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1216 BP; 405 A; 230 C; 258 G; 317 T; 6 other;

Query Match 37.8%; Score 1073.6; DB 24; Length 1216;
Best Local Similarity 96.2%; Pred. No. 1.7e-222;
Matches 1140; Conservative 0; Mismatches 39; Indels 6; Gaps 4;

QY 800 AAGGTGAAGCCCACTTTGGCAACGTATCTCAGCAAAAACTACAGCTATGTTATTCATGCC 859
Db 18 AAANAGAAGCCCACTTTGGCCCATATCNAGCAAAANCTACAGCTATGTTATTCATGCC 77
QY 860 AAATAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTGCACACGGTGTGGATGTAATA 919
Db 78 AAATAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTGCACACGGTGTGGATGTAATA 137
QY 920 GAGATCTTCAAGTCTCATCACCCATCCCTCGAAGCTCAAGTCCCGCTCATACAAATTC 979
Db 138 GAGATCTTCAAGTCTCATCACCCATCCCTCGAAGCTCAAGTCCCGCTCATACAAATTC 197
QY 980 TCTTCCAGTGTCCACACATCTTCCGCCCATCAAGATGTTCTCATCATGTGTTACGAGTGG 1039
Db 198 TCTTCCAGTGTCCACACATCTTCCGCCCATCAAGATGTTCTCATCATGTGTTACGAGTGG 257
QY 1040 CGTTCAAGGATGATGCTTCTTGAATAATGCTTAGTTGAAAAATGGAGAGATCAGCTTAGT 1099

Db 258 CGCTCAAGGATGATGCTTCTTTGAAATTCGTTAGTTGAAATGGAGAGATCAGCTTAGT 317
Qy 1100 AAAAGATCCATACAGTGGAGAGAGAGCTGCAGGAACAGCGGAGAACAGTTTCAGS--AC 1156
Db 318 AAAAGATCCATACAGTGGAGAGAGAGCTGCAGGAACAGCGGAGAACAGTTTCAGGGACAA 377
Qy 1157 AAGAAGAAACAGCGGGCGGCGCAGCTGTAATCCCGCCCAACCAAGGAAAGCCT 1216
Db 378 GAAAGAAACAGCGGGCGGCGCAGCTGTAATCCCGCCCAACCAAGGAAAGACT 437
Qy 1217 CCTGCTCCCAACAGCGGCGGCGCAGCTCCCAAGAAACATTTAAACTAGGAGTGCCCAAGAGA 1276
Db 438 CCTGCTCCCAACAGCGGCGGCGCAGCTCCCAAGAAACATTTAAACTAGGAGTGCCCAAGAGA 497
Qy 1277 ACAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAGACTTCCGACTTCCTTA 1336
Db 498 ACAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAGACTTCCGACTTCCTTA 557
Qy 1337 CAGGATGAGGCTGGGCAATTCCTGGGACAGCTATGTAAAGCCATGTGCCCTTTGCCCTA 1396
Db 558 CAGGATGAGGCTGGGCAATTCCTGGGACAGCTATGTAAAGCCATGTGCCCTTTGCCCTA 617
Qy 1397 ACAACTCACTGAGTGTCTTCATAGACACATCTTTGAGGCAATTTTCTTAAGGCTATGCT 1456
Db 618 ACAACTCACTGAGTGTCTTCATAGACACATCTTTGAGGCAATTTTCTTAAGGCTATGCT 677
Qy 1457 TCAGTTTTTCTTTGTAAGCCATCACAGCCATAGTGGTAGGTTTGGCCCTTTGGTACAGAA 1516
Db 678 TCAGTTTTTCTTTGTAAGCCATCACAGCCATAGTGGTAGGTTTGGCCCTTTGGTACAGAA 737
Qy 1517 GGTGAGTTAAAGCTGGTGGAAAGGCTTATTTGCATTTCAGAGTAACCTGTGTGCAT 1576
Db 738 GGTGAGTTAAAGCTGGTGGAAAGGCTTATTTGCATTTCAGAGTAACCTGTGTGCAT 797
Qy 1577 ACTCTAGAAGAGTAGGGGAAATTAATGCTTTGTTACAATTCGACCTTAATATGTGCATGTGAA 1636
Db 798 ACTCTAGAAGAGTAGGGGAAATTAATGCTTTGTTACAATTCGACCTTAATATGTGCATGTGAA 857
Qy 1637 AATAATGCCATATTTCAACCAACACAGTAATTTTTCAGATATGTTTTTATTACCTTT 1696
Db 858 AATAATGCCATATTTCAACCAACACAGTAATTTTTCAGATATGTTTTTATTACCTTT 917
Qy 1697 TGATATCTGTTGTCATGTTAGTGTATGTTTAAATGTGAT-GAAAAATATAATGTTTT 1755
Db 918 TGATATCTGTTGTCATGTTAGTGTATGTTTAAATGTGATCGAAATATAATGCTTC 977
Qy 1756 TAAGAAGAACAGTAGTGAATGAATGT-TAAAAAGATCTTTTATGTTTATGGTCCAG 1814
Db 978 TAAGAAGAACAGTAGTGAATGAATGTCTAAAAGATCTTTTATGTTTATGGTCCAG 1037
Qy 1815 AAGGATTTTGTGATGAAGGGGATTTTTCGAAAAAT-TAGAGAAGTAGCATATGGAATA 1873
Db 1038 AAGGATTTTGTGATGAAGGGGATTTTTCGAAAAATCTAGAGAAGTAGCATATGGAATA 1097
Qy 1874 TTATAATGCTGTTTTTTTACCAGTCTGCTGTTTTTGTCTGTTTTTGTCTAGAAAACTTAAAAAC 1933
Db 1098 TTATAATGCTGTTTTTTTACAGTACTCTGTTTTTGTCTAGAAAACTTAAAAAC 1157
Qy 1934 AAAAAATAATAAGAAAAATAATAAAAAAGGAGGAGGACAGACAA 1978
Db 1158 AAAAAATAATAAGAAAAATAATAAAAAAGGAGGAGGACAGNCAA 1202

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